

CLAIMS

We claim the following:

1. A hematopoietic protein comprising; an amino acid sequence of the formula:

$R_1-L_1-R_2$, $R_2-L_1-R_1$, R_1-R_2 , or R_2-R_1

wherein R_1 and R_2 are independently selected from the group consisting of:

(I) A polypeptide comprising a modified human G-CSF amino acid sequence selected from the group consisting of:

(a) an amino acid sequence of the formula:

1	10
Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa	
20	
Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly	
30	40
Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa	
50	
Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp	
60	70
Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly	
80	
Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu	
90	100
Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu	
110	
Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp	
120	130
Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr	

40
41 140
42 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala
43
44 150 160
45 Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa
46
47 170
48 Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro (SEQ ID NO:1)
49
50 wherein
51
52 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
53 Xaa at position 2 is Pro or Leu;
54 Xaa at position 3 is Leu, Arg, Tyr or Ser;
55 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
56 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
57 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or
58 Arg;
59 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
60 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
61 Xaa at position 24 is Ile, Pro, Tyr or Leu;
62 Xaa at position 27 is Asp, or Gly;
63 Xaa at position 30 is Ala, Ile, Leu or Gly;
64 Xaa at position 34 is Lys or Ser;
65 Xaa at position 36 is Cys or Ser;
66 Xaa at position 42 is Cys or Ser;
67 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
68 Arg, Cys, or Leu;
69 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
70 Trp, Gln, or Thr;
71 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
72 Xaa at position 47 is Leu or Thr;
73 Xaa at position 49 is Leu, Phe, Arg or Ser;
74 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
75 Xaa at position 54 is Leu or His;
76 Xaa at position 64 is Cys or Ser;
77 Xaa at position 67 is Gln, Lys, Leu or Cys;
78 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
79 Xaa at position 74 is Cys or Ser;
80 Xaa at position 104 is Asp, Gly or Val;
81 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
82 Gly;
83 Xaa at position 115 is Thr, His, Leu or Ala;
84 Xaa at position 120 is Gln, Gly, Arg, Lys or His
85 Xaa at position 123 is Glu, Arg, Phe or Thr
86 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or

87 Glu;

88 Xaa at position 146 is Arg or Gln;

89 Xaa at position 147 is Arg or Gln;

90 Xaa at position 156 is His, Gly or Ser;

91 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;

92 Xaa at position 162 is Glu, Leu, Gly or Trp;

93 Xaa at position 163 is Val, Gly, Arg or Ala;

94 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;

95 Xaa at position 170 is His, Arg or Ser;

96

97 wherein optionally 1-11 amino acids from the N-terminus and 1-

98 5 from the C-terminus can optionally be deleted from said

99 modified human G-CSF amino acid sequence; and

100

101 wherein the N-terminus is joined to the C-terminus directly or

102 through a linker capable of joining the N-terminus to the C-

103 terminus and having new C- and N-termini at amino acids:

104

105

106 38-39

62-63

123-124

107 39-40

63-64

124-125

108 40-41

64-65

125-126

109 41-42

65-66

126-127

110 42-43

66-67

128-129

111 43-44

67-68

128-129

112 45-46

68-69

129-130

113 48-49

69-70

130-131

114 49-50

70-71

131-132

115 52-53

71-72

132-133

116 53-54

91-92

133-134

117 54-55

92-93

134-135

118 55-56

93-94

135-136

119 56-57

94-95

136-137

120 57-58

95-96

137-138

121 58-59

96-97

138-139

122 59-60

97-98

139-140

123 60-61

98-99

140-141

124 61-62

99-100

141-142

125

or 142-143

126

respectively; and

127

128 (b) an amino acid sequence of the formula:

129

130 1

10

131 Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

132

133 20
134 Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly
135
136 30 40
137 Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa
138
139 50
140 Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp
141
142 60 70
143 Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly
144
145 80
146 Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
147
148 90 100
149 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
150
151 110
152 Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp
153
154 120 130
155 Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr
156
157 140
158 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala
159
160 150 160
161 Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa
162
163 170
164 Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro (SEQ ID NO:1)
165
166 wherein
167
168 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
169 Xaa at position 2 is Pro or Leu;
170 Xaa at position 3 is Leu, Arg, Tyr or Ser;
171 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
172 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
173 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or
174 Arg;
175 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
176 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
177 Xaa at position 24 is Ile, Pro, Tyr or Leu;
178 Xaa at position 27 is Asp, or Gly;
179 Xaa at position 30 is Ala, Ile, Leu or Gly;

180 Xaa at position 34 is Lys or Ser;
181 Xaa at position 36 is Cys or Ser;
182 Xaa at position 42 is Cys or Ser;
183 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
184 Arg, Cys, or Leu;
185 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
186 Trp, Gln, or Thr;
187 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
188 Xaa at position 47 is Leu or Thr;
189 Xaa at position 49 is Leu, Phe, Arg or Ser;
190 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
191 Xaa at position 54 is Leu or His;
192 Xaa at position 64 is Cys or Ser;
193 Xaa at position 67 is Gln, Lys, Leu or Cys;
194 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
195 Xaa at position 74 is Cys or Ser;
196 Xaa at position 104 is Asp, Gly or Val;
197 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
198 Gly;
199 Xaa at position 115 is Thr, His, Leu or Ala;
200 Xaa at position 120 is Gln, Gly, Arg, Lys or His
201 Xaa at position 123 is Glu, Arg, Phe or Thr
202 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
203 Glu;
204 Xaa at position 146 is Arg or Gln;
205 Xaa at position 147 is Arg or Gln;
206 Xaa at position 156 is His, Gly or Ser;
207 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
208 Xaa at position 162 is Glu, Leu, Gly or Trp;
209 Xaa at position 163 is Val, Gly, Arg or Ala;
210 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
211 Xaa at position 170 is His, Arg or Ser,
212
213
214 wherein optionally 1-11 amino acids from the N-terminus and 1-
215 5 from the C-terminus can be deleted;
216
217 wherein the N-terminus is joined to the C-terminus directly or
218 through a linker capable of joining the N-terminus to the C-
219 terminus and having new C- and N-terminus at amino acids:
220
221 2-3
222 10-11
223 12-13
224 18-19

225 122-123
 226 158-159
 227 169-170;

228

229 (II) A polypeptide comprising; a modified human IL-3
 230 amino acid sequence of the formula:

231

232

233 Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
 234 1 5 10 15

235

236 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 237 20 25 30

238

239 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
 240 35 40 45

241

242 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 243 50 55 60

244

245 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 246 65 70 75

247

248 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 249 80 85 90

250

251 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 252 95 100 105

253

254 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 255 110 115 120

256

257 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
 258 125 130 (SEQ ID NO:2)

259

260 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
261 Arg;
262 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
263 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
264 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
265 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
266 Asn, Thr, Ser or Val;
267 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
268 Gln, Leu, Val or Gly;
269 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
270 Leu, Ser, or Arg;
271 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
272 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
273 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
274 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
275 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
276 Trp;
277 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
278 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
279 or Lys;
280 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
281 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
282 Glu;
283 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
284 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
285 Arg, Ala, Phe, Ile or Met;
286 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
287 Xaa at position 36 is Asp, Leu, or Val;
288 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
289 Xaa at position 38 is Asn, or Ala;
290 Xaa at position 40 is Leu, Trp, or Arg;
291 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
292 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
293 Val, Glu, Phe, Tyr, Ile, Met or Ala;
294 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
295 Gln, Arg, Thr, Gly or Ser;

296 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
297 Glu, Asn, Gln, Ala or Pro;
298 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
299 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
300 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
301 Lys, His, Ala, Tyr, Ile, Val or Gly;
302 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
303 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
304 Lys, Thr, Ala, Met, Val or Asn;
305 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
306 Asp;
307 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
308 Ala, Ile, Val, His, Phe, Met or Gln;
309 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
310 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
311 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
312 or Met;
313 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
314 Lys, His, Ala or Leu;
315 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
316 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
317 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
318 Xaa at position 57 is Asn or Gly;
319 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
320 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
321 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
322 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
323 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
324 Ile;
325 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
326 Val;
327 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
328 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
329 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
330 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
331 or

332 His;
333 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
334 His;
335 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
336 or Leu;
337 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
338 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
339 Trp, or Asn;
340 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
341 Asp;
342 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
343 Arg;
344 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
345 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
346 Gln, or Leu;
347 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
348 or
349 Asp;
350 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
351 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
352 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
353 Asp;
354 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
355 Arg;
356 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
357 Lys;
358 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
359 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
360 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
361 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
362 Xaa at position 85 is Leu, Asn, Val, or Gln;
363 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
364 Xaa at position 87 is Leu, Ser, Trp, or Gly;
365 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
366 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
367 or Ser;

368 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
369 Met;
370 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
371 His;
372 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
373 Ile or Leu;
374 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
375 Arg;
376 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
377 His, Ala, or Pro;
378 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
379 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
380 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
381 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
382 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
383 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
384 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
385 Gly, Ser, Phe, or His;
386 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
387 or Pro;
388 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
389 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
390 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
391 Xaa at position 103 is Asp, or Ser;
392 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
393 Gln, Lys, Ala, Phe, or Gly;
394 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
395 Leu, Lys, Ile, Asp, or His;
396 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
397 Pro;
398 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
399 Ser, Ala or Pro;
400 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
401 Gly;
402 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
403 Glu, Ser, or Trp;

404 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
405 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
406 Phe;
407 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
408 Lys, Leu, Ile, Val or Asn;
409 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
410 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
411 Trp, or Met;
412 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
413 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
414 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
415 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
416 Tyr;
417 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
418 Arg;
419 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
420 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
421 Gly;
422 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
423 Ile, Tyr, or Cys;
424 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
425 Leu;
426
427 wherein from 1 to 14 amino acids can optionally be deleted
428 from the N-terminus and/or from 1 to 15 amino acids can
429 optionally be deleted from the C-terminus of said modified
430 human IL-3 amino acid sequence; wherein from 0 to 44 of the
431 amino acids designated by Xaa are different from the
432 corresponding amino acids of native (1-133) human interleukin-
433 3; and
434
435 wherein the N-terminus is joined to the C-terminus directly or
436 through a linker (L₂), capable of joining the N-terminus to
437 the C-terminus and having new C- and N-termini at amino acids:
438

438

26-27	49-50	83-84
27-28	50-51	84-85
28-29	51-52	85-86
29-30	52-53	86-87
30-31	53-54	87-88
31-32	54-55	88-89
32-33	64-65	89-90
33-34	65-66	90-91
34-35	66-67	91-92
35-36	67-68	92-93
36-37	68-69	97-98
37-38	69-70	98-99
38-39	70-71	99-100
39-40	71-72	100-101
40-41	72-73	101-102
41-42	82-83	102-103
		or 103-104 respectively;

439

440

441 (III) A polypeptide comprising; a modified human c-mpl
 442 ligand amino acid sequence selected from the group consisting
 443 of:

444

445 (a) an amino acid sequence of the formula:

446

447 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer

448 1 5 10 15

449

450 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro

451 20 25 30 35

452

453 ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu

454 40 45 50 55

455

456 ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla

457 60 65 70 75

458

459 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly

460 80 85 90 95

461

462 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa

463 100 105 110

464
 465 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 466 115 120 125 130
 467
 468 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
 469 135 140 145 150
 470
 471 Arg (SEQ ID NO:256)
 472 153
 473
 474 wherein
 475
 476 Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro,
 477 Phe, Trp, or Met;
 478 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 479 Ile, Trp, or Met;
 480 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 481 Ile, Trp, or Met;
 482 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 483 Asn; and
 484
 485 wherein the N-terminus is joined to the C-terminus directly or
 486 through a linker (L2) capable of joining the N-terminus to the
 487 C-terminus and having new C- and N-termini at amino acids:
 488

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124

46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127
50-51	88-89	or 127-128 respectively; and

489

490 (b) an amino acid sequence of the formula:

491

492 SerProAlaProProAlaXaaAspLeuArgValLeuSerLysLeuLeuArgAspSer

493 1 5 10 15

494

495 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro

496 20 25 30 35

497

498 ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu

499 40 45 50 55

500

501 ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla

502 60 65 70 75

503

504 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly

505 80 85 90 95

506

507 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa

508 100 105 110

509

510 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis

511 115 120 125 130

512

513 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuXaaVal

514 135 140 145 150

515

516 Arg (SEQ ID NO:283)

517 153

518

519 wherein

520 Xaa at position 7 is Ser or Ala;

521 Xaa at position 112 is deleted or Leu, Ala, Val, Ile,

522 Pro, Phe, Trp, or Met;

523 Xaa at position 113 is deleted or Pro, Phe, Ala, Val,

524 Leu, Ile, Trp, or Met;

525 Xaa at position 114 is deleted or Pro, Phe, Ala, Val,

526 Leu, Ile, Trp, or Met;

527 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr,
 528 Tyr, or Asn;
 529 Xaa at position 151 is Ser or Ala,
 530
 531 wherein the N-terminus is joined to the C-terminus directly or
 532 through a linker capable of joining the N-terminus to the C-
 533 terminus and having new C- and N-termini at amino acids:
 534

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127
50-51	88-89	or 127-128;

535
 536 (IV) A polypeptide comprising; a modified human IL-3
 537 amino acid sequence of the formula:
 538
 539 Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
 540 1 5 10 15
 541
 542 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 543 20 25 30
 544
 545 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
 546 35 40 45

547
 548 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 549 50 55 60
 550
 551 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 552 65 70 75
 553
 554 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 555 80 85 90
 556
 557 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 558 95 100 105
 559
 560 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 561 110 115 120
 562
 563 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
 564 125 130 (SEQ ID NO:2)
 565
 566 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
 567 Arg;
 568 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
 569 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
 570 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
 571 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
 572 Asn, Thr, Ser or Val;
 573 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
 574 Gln, Leu, Val or Gly;
 575 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
 576 Leu, Ser, or Arg;
 577 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
 578 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
 579 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
 580 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
 581 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
 582 Trp;

583 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
584 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
585 or Lys;
586 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
587 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
588 Glu;
589 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
590 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
591 Arg, Ala, Phe, Ile or Met;
592 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
593 Xaa at position 36 is Asp, Leu, or Val;
594 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
595 Xaa at position 38 is Asn, or Ala;
596 Xaa at position 40 is Leu, Trp, or Arg;
597 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
598 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
599 Val, Glu, Phe, Tyr, Ile, Met or Ala;
600 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
601 Gln, Arg, Thr, Gly or Ser;
602 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
603 Glu, Asn, Gln, Ala or Pro;
604 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
605 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
606 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
607 Lys, His, Ala, Tyr, Ile, Val or Gly;
608 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
609 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
610 Lys, Thr, Ala, Met, Val or Asn;
611 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
612 Asp;
613 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
614 Ala, Ile, Val, His, Phe, Met or Gln;
615 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
616 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
617 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
618 or Met;

619 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
620 Lys, His, Ala or Leu;
621 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
622 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
623 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
624 Xaa at position 57 is Asn or Gly;
625 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
626 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
627 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
628 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
629 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
630 Ile;
631 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
632 Val;
633 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
634 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
635 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
636 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
637 or His;
638 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
639 His;
640 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
641 or Leu;
642 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
643 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
644 Trp, or Asn;
645 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
646 Asp;
647 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
648 Arg;
649 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
650 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
651 Gln, or Leu;
652 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
653 or
654 Asp;

655 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
656 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
657 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
658 Asp;
659 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
660 Arg;
661 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
662 Lys;
663 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
664 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
665 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
666 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
667 Xaa at position 85 is Leu, Asn, Val, or Gln;
668 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
669 Xaa at position 87 is Leu, Ser, Trp, or Gly;
670 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
671 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
672 or Ser;
673 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
674 Met;
675 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
676 His;
677 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
678 Ile or Leu;
679 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
680 Arg;
681 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
682 His, Ala, or Pro;
683 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
684 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
685 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
686 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
687 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
688 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
689 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
690 Gly, Ser, Phe, or His;

691 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
692 or Pro;
693 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
694 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
695 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
696 Xaa at position 103 is Asp, or Ser;
697 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
698 Gln, Lys, Ala, Phe, or Gly;
699 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
700 Leu, Lys, Ile, Asp, or His;
701 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
702 Pro;
703 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
704 Ser, Ala or Pro;
705 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
706 Gly;
707 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
708 Glu, Ser, or Trp;
709 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
710 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
711 Phe;
712 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
713 Lys, Leu, Ile, Val or Asn;
714 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
715 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
716 Trp, or Met;
717 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
718 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
719 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
720 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
721 Tyr;
722 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
723 Arg;
724 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
725 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
726 Gly;

727 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
728 Ile, Tyr, or Cys;

729 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
730 Leu,

731
732 wherein from 1 to 14 amino acids can optionally be deleted
733 from the N-terminus and/or from 1 to 15 amino acids can
734 optionally be deleted from the C-terminus of said modified
735 human IL-3 amino acid sequence; and wherein from 1 to 44 of
736 the amino acids designated by Xaa are different from the
737 corresponding amino acids of native (1-133) human interleukin-
738 3; and

739
740
741 (V) a colony stimulating factor;

742
743 and wherein L₁ is a linker capable of linking R₁ to R₂;

744
745 with the proviso that at least R₁ or R₂ is selected from
746 the polypeptide of formula (I) , (II), or (III); and

747
748 said hematopoietic protein can optionally be immediately
749 preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻², alanine⁻
750 1).

1 2. A hematopoietic protein comprising; an amino acid sequence
2 of the formula:

3
4 R₁-L₁-R₂, R₂-L₁-R₁, R₁-R₂, or R₂-R₁

5
6 wherein R₁ and R₂ are independently selected from the
7 group consisting of:

8
9 (I) A polypeptide comprising; a modified human G-CSF
10 amino acid sequence of the formula:

11

12 1 10
13 Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa
14
15 20
16 Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly
17
18 30 40
19 Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa
20
21 50
22 Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp
23
24 60 70
25 Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly
26
27 80
28 Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
29
30 90 100
31 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
32
33 110
34 Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp
35
36 120 130
37 Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr
38
39 140
40 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala
41
42 150 160
43 Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa
44
45 170
46 Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro (SEQ ID NO:1)
47

48 wherein

49
50 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
51 Xaa at position 2 is Pro or Leu;
52 Xaa at position 3 is Leu, Arg, Tyr or Ser;
53 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
54 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
55 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;
56 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
57 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
58 Xaa at position 24 is Ile, Pro, Tyr or Leu;

59 Xaa at position 27 is Asp, or Gly;
60 Xaa at position 30 is Ala, Ile, Leu or Gly;
61 Xaa at position 34 is Lys or Ser;
62 Xaa at position 36 is Cys or Ser;
63 Xaa at position 42 is Cys or Ser;
64 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
65 Arg, Cys, or Leu;
66 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
67 Trp, Gln, or Thr;
68 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
69 Xaa at position 47 is Leu or Thr;
70 Xaa at position 49 is Leu, Phe, Arg or Ser;
71 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
72 Xaa at position 54 is Leu or His;
73 Xaa at position 64 is Cys or Ser;
74 Xaa at position 67 is Gln, Lys, Leu or Cys;
75 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
76 Xaa at position 74 is Cys or Ser;
77 Xaa at position 104 is Asp, Gly or Val;
78 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
79 Gly;
80 Xaa at position 115 is Thr, His, Leu or Ala;
81 Xaa at position 120 is Gln, Gly, Arg, Lys or His
82 Xaa at position 123 is Glu, Arg, Phe or Thr
83 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
84 Glu;
85 Xaa at position 146 is Arg or Gln;
86 Xaa at position 147 is Arg or Gln;
87 Xaa at position 156 is His, Gly or Ser;
88 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
89 Xaa at position 162 is Glu, Leu, Gly or Trp;
90 Xaa at position 163 is Val, Gly, Arg or Ala;
91 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
92 Xaa at position 170 is His, Arg or Ser,
93
94 wherein optionally 1-11 amino acids from the N-terminus and 1-
95 5 from the C-terminus can optionally be deleted from said
96 modified human G-CSF amino acid sequence; and
97
98 wherein the N-terminus is joined to the C-terminus directly or
99 through a linker capable of joining the N-terminus to the C-
100 terminus and having new C- and N-termini at amino acids;
101
102
103 38-39 62-63 123-124
104 39-40 63-64 124-125

105	40-41	64-65	125-126
106	41-42	65-66	126-127
107	42-43	66-67	128-129
108	43-44	67-68	128-129
109	45-46	68-69	129-130
110	48-49	69-70	130-131
111	49-50	70-71	131-132
112	52-53	71-72	132-133
113	53-54	91-92	133-134
114	54-55	92-93	134-135
115	55-56	93-94	135-136
116	56-57	94-95	136-137
117	57-58	95-96	137-138
118	58-59	96-97	138-139
119	59-60	97-98	139-140
120	60-61	98-99	140-141
121	61-62	99-100	141-142
122			or 142-143
123			respectively;
124			

125 (II) A polypeptide comprising; a modified human IL-3
 126 amino acid sequence of the formula:

127															
128	Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn
129	1				5					10					15
130															
131	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
132					20					25					30
133															
134	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
135					35					40					45
136															
137	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
138					50					55					60
139															
140	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
141					65					70					75
142															
143	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
144					80					85					90

145
146 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
147 95 100 105
148
149 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
150 110 115 120
151
152 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
153 125 130 (SEQ ID NO:2)
154
155 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
156 Arg;
157 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
158 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
159 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
160 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
161 Asn,
162 Thr, Ser or Val;
163 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
164 Gln,
165 Leu, Val or Gly;
166 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
167 Leu, Ser, or Arg;
168 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
169 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
170 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
171 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
172 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
173 Trp;
174 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
175 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
176 or Lys;
177 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
178 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
179 Glu;
180 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;

181 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
182 Arg, Ala, Phe, Ile or Met;
183 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
184 Xaa at position 36 is Asp, Leu, or Val;
185 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
186 Xaa at position 38 is Asn, or Ala;
187 Xaa at position 40 is Leu, Trp, or Arg;
188 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
189 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
190 Val, Glu, Phe, Tyr, Ile, Met or Ala;
191 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
192 Gln, Arg, Thr, Gly or Ser;
193 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
194 Glu, Asn, Gln, Ala or Pro;
195 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
196 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
197 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
198 Lys, His, Ala, Tyr, Ile, Val or Gly;
199 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
200 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
201 Lys, Thr, Ala, Met, Val or Asn;
202 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
203 Asp;
204 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
205 Ala, Ile, Val, His, Phe, Met or Gln;
206 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
207 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
208 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
209 or Met;
210 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
211 Lys, His, Ala or Leu;
212 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
213 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
214 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
215 Xaa at position 57 is Asn or Gly;
216 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;

217 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
218 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
219 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
220 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
221 Ile;
222 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
223 Val;
224 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
225 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
226 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
227 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
228 or His;
229 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
230 His;
231 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
232 or Leu;
233 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
234 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
235 Trp, or Asn;
236 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
237 Asp;
238 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
239 Arg;
240 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
241 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
242 Gln, or Leu;
243 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
244 or Asp;
245 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
246 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
247 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
248 Asp;
249 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
250 Arg;
251 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
252 Lys;

253 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
254 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
255 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
256 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
257 Xaa at position 85 is Leu, Asn, Val, or Gln;
258 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
259 Xaa at position 87 is Leu, Ser, Trp, or Gly;
260 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
261 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
262 or Ser;
263 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
264 Met;
265 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
266 His;
267 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
268 Ile Leu;
269 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
270 Arg;
271 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
272 His, Ala, or Pro;
273 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
274 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
275 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
276 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
277 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
278 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
279 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
280 Gly, Ser, Phe, or His;
281 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
282 or Pro;
283 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
284 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
285 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
286 Xaa at position 103 is Asp, or Ser;
287 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
288 Gln, Lys, Ala, Phe, or Gly;

289 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
290 Leu, Lys, Ile, Asp, or His;
291 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
292 Pro;
293 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
294 Ser, Ala or Pro;
295 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
296 Gly;
297 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
298 Glu, Ser, or Trp;
299 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
300 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
301 Phe;
302 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
303 Lys, Leu, Ile, Val or Asn;
304 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
305 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
306 Trp, or Met;
307 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
308 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
309 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
310 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
311 Tyr;
312 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
313 Arg;
314 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
315 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
316 Gly;
317 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
318 Ile, Tyr, or Cys;
319 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
320 Leu,
321
322 wherein from 1 to 14 amino acids can optionally be deleted
323 from the N-terminus and/or from 1 to 15 amino acids can
324 optionally be deleted from the C-terminus of said modified

human IL-3 amino acid sequence; wherein from 0 to 44 of the amino acids designated by Xaa are different from the corresponding amino acids of native (1-133) human interleukin-3; and

wherein the N-terminus is joined to the C-terminus directly or through a linker (L₂), capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids:

26-27	49-50	83-84
27-28	50-51	84-85
28-29	51-52	85-86
29-30	52-53	86-87
30-31	53-54	87-88
31-32	54-55	88-89
32-33	64-65	89-90
33-34	65-66	90-91
34-35	66-67	91-92
35-36	67-68	92-93
36-37	68-69	97-98
37-38	69-70	98-99
38-39	70-71	99-100
39-40	71-72	100-101
40-41	72-73	101-102
41-42	82-83	102-103
		or 103-104 respectively;

334
335

(III) A polypeptide comprising; a modified human c-mpl ligand amino acid sequence of the formula:

338

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1 5 10 15

341

HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
20 25 30 35

344

ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
40 45 50 55

347

ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
60 65 70 75

349

350
 351 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
 352 80 85 90 95
 353
 354 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
 355 100 105 110
 356
 357 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 358 115 120 125 130
 359
 360 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
 361 135 140 145 150
 362
 363 Arg (SEQ ID NO:256)
 364 153
 365
 366 wherein
 367
 368 Xaa at position 112 is deleted or Leu, Ala, Val, Ile,
 369 Pro, Phe, Trp, or Met;
 370 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 371 Ile, Trp, or Met;
 372 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 373 Ile, Trp, or Met;
 374 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 375 Asn,
 376
 377 wherein the N-terminus is joined to the C-terminus directly or
 378 through a linker (L2) capable of joining the N-terminus to the
 379 C-terminus and having new C- and N-termini at amino acids:

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118

38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127
50-51	88-89	or 127-128 respectively;

381

382

383 (IV) A polypeptide comprising; a modified human IL-3
 384 amino acid sequence of the formula:

385

386

387 Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
 388 1 5 10 15

389

390 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 391 20 25 30

392

393 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
 394 35 40 45

395

396 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 397 50 55 60

398

399 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 400 65 70 75

401

402 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 403 80 85 90

404

405 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 406 95 100 105

407

408 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
409 110 115 120
410
411 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
412 125 130 (SEQ ID NO:2)
413
414 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
415 Arg;
416 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
417 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
418 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
419 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
420 Asn,
421 Thr, Ser or Val;
422 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
423 Gln,
424 Leu, Val or Gly;
425 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
426 Leu, Ser, or Arg;
427 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
428 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
429 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
430 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
431 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
432 Trp;
433 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
434 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
435 or Lys;
436 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
437 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
438 Glu;
439 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
440 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
441 Arg, Ala, Phe, Ile or Met;
442 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
443 Xaa at position 36 is Asp, Leu, or Val;

444 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
445 Xaa at position 38 is Asn, or Ala;
446 Xaa at position 40 is Leu, Trp, or Arg;
447 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
448 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
449 Val, Glu, Phe, Tyr, Ile, Met or Ala;
450 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
451 Gln, Arg, Thr, Gly or Ser;
452 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
453 Glu, Asn, Gln, Ala or Pro;
454 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
455 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
456 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
457 Lys, His, Ala, Tyr, Ile, Val or Gly;
458 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
459 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
460 Lys, Thr, Ala, Met, Val or Asn;
461 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
462 Asp;
463 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
464 Ala, Ile, Val, His, Phe, Met or Gln;
465 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
466 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
467 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
468 or Met;
469 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
470 Lys, His, Ala or Leu;
471 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
472 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
473 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
474 Xaa at position 57 is Asn or Gly;
475 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
476 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
477 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
478 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;

479 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
480 Ile;
481 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
482 Val;
483 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
484 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
485 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
486 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
487 or His;
488 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
489 His;
490 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
491 or Leu;
492 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
493 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
494 Trp, or Asn;
495 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
496 Asp;
497 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
498 Arg;
499 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
500 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
501 Gln, or Leu;
502 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
503 or Asp;
504 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
505 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
506 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
507 Asp;
508 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
509 Arg;
510 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
511 Lys;
512 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
513 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
514 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;

515 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
516 Xaa at position 85 is Leu, Asn, Val, or Gln;
517 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
518 Xaa at position 87 is Leu, Ser, Trp, or Gly;
519 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
520 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
521 or Ser;
522 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
523 Met;
524 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
525 His;
526 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
527 Ile or Leu;
528 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
529 Arg;
530 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
531 His, Ala, or Pro;
532 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
533 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
534 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
535 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
536 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
537 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
538 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
539 Gly, Ser, Phe, or His;
540 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
541 or Pro;
542 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
543 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
544 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
545 Xaa at position 103 is Asp, or Ser;
546 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
547 Gln, Lys, Ala, Phe, or Gly;
548 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
549 Leu, Lys, Ile, Asp, or His;

550 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
551 Pro;
552 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
553 Ser, Ala or Pro;
554 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
555 Gly;
556 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
557 Glu, Ser, or Trp;
558 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
559 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
560 Phe;
561 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
562 Lys, Leu, Ile, Val or Asn;
563 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
564 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
565 Trp, or Met;
566 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
567 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
568 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
569 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
570 Tyr;
571 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
572 Arg;
573 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
574 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
575 Gly;
576 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
577 Ile, Tyr, or Cys;
578 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
579 Leu;
580
581 wherein from 1 to 14 amino acids can optionally be deleted
582 from the N-terminus and/or from 1 to 15 amino acids can
583 optionally be deleted from the C-terminus of said modified
584 human IL-3 amino acid sequence; and wherein from 1 to 44 of
585 the amino acids designated by Xaa are different from the

26
27 80
28 Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
29
30 90 100
31 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
32
33 110
34 Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp
35
36 120 130
37 Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr
38
39 140
40 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala
41
42 150 160
43 Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa
44
45 170
46 Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro (SEQ ID NO:1)
47

48 wherein

49
50 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
51 Xaa at position 2 is Pro or Leu;
52 Xaa at position 3 is Leu, Arg, Tyr or Ser;
53 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
54 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
55 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or
56 Arg;
57 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
58 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
59 Xaa at position 24 is Ile, Pro, Tyr or Leu;
60 Xaa at position 27 is Asp, or Gly;
61 Xaa at position 30 is Ala, Ile, Leu or Gly;
62 Xaa at position 34 is Lys or Ser;
63 Xaa at position 36 is Cys or Ser;
64 Xaa at position 42 is Cys or Ser;
65 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
66 Arg, Cys, or Leu;
67 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
68 Trp, Gln, or Thr;
69 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
70 Xaa at position 47 is Leu or Thr;
71 Xaa at position 49 is Leu, Phe, Arg or Ser;
72 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;

73 Xaa at position 54 is Leu or His;
74 Xaa at position 64 is Cys or Ser;
75 Xaa at position 67 is Gln, Lys, Leu or Cys;
76 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
77 Xaa at position 74 is Cys or Ser;
78 Xaa at position 104 is Asp, Gly or Val;
79 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
80 Gly;
81 Xaa at position 115 is Thr, His, Leu or Ala;
82 Xaa at position 120 is Gln, Gly, Arg, Lys or His
83 Xaa at position 123 is Glu, Arg, Phe or Thr
84 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
85 Glu;
86 Xaa at position 146 is Arg or Gln;
87 Xaa at position 147 is Arg or Gln;
88 Xaa at position 156 is His, Gly or Ser;
89 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
90 Xaa at position 162 is Glu, Leu, Gly or Trp;
91 Xaa at position 163 is Val, Gly, Arg or Ala;
92 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
93 Xaa at position 170 is His, Arg or Ser,
94
95 wherein optionally 1-11 amino acids from the N-terminus and 1-
96 5 from the C-terminus can be deleted from said modified human
97 G-CSF amino acid sequence; and
98
99 wherein the N-terminus is joined to the C-terminus directly or
100 through a linker capable of joining the N-terminus to the C-
101 terminus and having new C- and N-termini at amino acids:
102
103
104 38-39 62-63 123-124
105 39-40 63-64 124-125
106 40-41 64-65 125-126
107 41-42 65-66 126-127
108 42-43 66-67 128-129
109 43-44 67-68 128-129
110 45-46 68-69 129-130
111 48-49 69-70 130-131
112 49-50 70-71 131-132
113 52-53 71-72 132-133
114 53-54 91-92 133-134
115 54-55 92-93 134-135
116 55-56 93-94 135-136
117 56-57 94-95 136-137
118 57-58 95-96 137-138

119	58-59	96-97	138-139
120	59-60	97-98	139-140
121	60-61	98-99	140-141
122	61-62	99-100	141-142
123			or 142-143
124			respectively;
125			
126			

127 (II) A polypeptide comprising; a modified human IL-3
 128 amino acid sequence of the formula:

129
 130

131	Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn
132	1				5					10					15
133															
134	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
135					20					25					30
136															
137	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
138					35					40					45
139															
140	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
141					50					55					60
142															
143	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
144					65					70					75
145															
146	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
147					80					85					90
148															
149	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
150					95					100					105
151															
152	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
153					110					115					120
154															
155	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe		

156 125 130 (SEQ ID NO:2)
157
158 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
159 Arg;
160 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
161 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
162 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
163 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
164 Asn,
165 Thr, Ser or Val;
166 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
167 Gln,
168 Leu, Val or Gly;
169 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
170 Leu, Ser, or Arg;
171 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
172 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
173 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
174 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
175 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
176 Trp;
177 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
178 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
179 or Lys;
180 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
181 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
182 Glu;
183 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
184 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
185 Arg, Ala, Phe, Ile or Met;
186 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
187 Xaa at position 36 is Asp, Leu, or Val;
188 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
189 Xaa at position 38 is Asn, or Ala;
190 Xaa at position 40 is Leu, Trp, or Arg;
191 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;

192 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
193 Val, Glu, Phe, Tyr, Ile, Met or Ala;
194 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
195 Gln, Arg, Thr, Gly or Ser;
196 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
197 Glu, Asn, Gln, Ala or Pro;
198 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
199 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
200 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
201 Lys, His, Ala, Tyr, Ile, Val or Gly;
202 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
203 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
204 Lys, Thr, Ala, Met, Val or Asn;
205 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
206 Asp;
207 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
208 Ala, Ile, Val, His, Phe, Met or Gln;
209 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
210 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
211 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
212 or Met;
213 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
214 Lys, His, Ala or Leu;
215 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
216 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
217 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
218 Xaa at position 57 is Asn or Gly;
219 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
220 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
221 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
222 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
223 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
224 Ile;
225 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
226 Val;
227 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;

228 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
229 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
230 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
231 or His;
232 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
233 His;
234 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
235 or Leu;
236 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
237 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
238 Trp, or Asn;
239 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
240 Asp;
241 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
242 Arg;
243 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
244 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
245 Gln, or Leu;
246 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
247 or Asp;
248 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
249 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
250 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
251 Asp;
252 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
253 Arg;
254 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
255 Lys;
256 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
257 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
258 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
259 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
260 Xaa at position 85 is Leu, Asn, Val, or Gln;
261 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
262 Xaa at position 87 is Leu, Ser, Trp, or Gly;
263 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;

264 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
265 or Ser;
266 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
267 Met;
268 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
269 His;
270 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
271 Ile or Leu;
272 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
273 Arg;
274 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
275 His, Ala, or Pro;
276 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
277 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
278 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
279 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
280 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
281 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
282 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
283 Gly, Ser, Phe, or His;
284 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
285 or Pro;
286 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
287 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
288 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
289 Xaa at position 103 is Asp, or Ser;
290 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
291 Gln, Lys, Ala, Phe, or Gly;
292 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
293 Leu, Lys, Ile, Asp, or His;
294 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
295 Pro;
296 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
297 Ser, Ala or Pro;
298 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
299 Gly;

300 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
301 Glu, Ser, or Trp;
302 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
303 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
304 Phe;
305 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
306 Lys, Leu, Ile, Val or Asn;
307 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
308 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
309 Trp, or Met;
310 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
311 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
312 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
313 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
314 Tyr;
315 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
316 Arg;
317 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
318 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
319 Gly;
320 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
321 Ile, Tyr, or Cys;
322 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
323 Leu,
324
325 wherein from 1 to 14 amino acids can optionally be deleted
326 from the N-terminus and/or from 1 to 15 amino acids can
327 optionally be deleted from the C-terminus of said modified
328 human IL-3 amino acid sequence; and wherein from 0 to 44 of
329 the amino acids designated by Xaa are different from the
330 corresponding amino acids of native (1-133) human interleukin-
331 3; and
332
333 wherein the N-terminus is joined to the C-terminus directly or
334 through a linker (L₂) capable of joining the N-terminus to the
335 C-terminus and having new C- and N-termini at amino acids:

336

26-27	49-50	83-84
27-28	50-51	84-85
28-29	51-52	85-86
29-30	52-53	86-87
30-31	53-54	87-88
31-32	54-55	88-89
32-33	64-65	89-90
33-34	65-66	90-91
34-35	66-67	91-92
35-36	67-68	92-93
36-37	68-69	97-98
37-38	69-70	98-99
38-39	70-71	99-100
39-40	71-72	100-101
40-41	72-73	101-102
41-42	82-83	102-103
		or 103-104 respectively;

337

338

339 (III) A polypeptide comprising; a modified human c-mpl
 340 ligand amino acid sequence of the formula:

341

342 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
 343 1 5 10 15

344

345 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
 346 20 25 30 35

347

348 ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
 349 40 45 50 55

350

351 ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
 352 60 65 70 75

353

354 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
 355 80 85 90 95

356

357 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
 358 100 105 110

359

360 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 361 115 120 125 130

362
 363 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
 364 135 140 145 150
 365
 366 Arg (SEQ ID NO:256)
 367 153
 368
 369 wherein
 370
 371 Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro,
 372 Phe, Trp, or Met;
 373 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 374 Ile, Trp, or Met;
 375 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 376 Ile, Trp, or Met;
 377 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 378 Asn; and
 379
 380 wherein the N-terminus is joined to the C-terminus directly or
 381 through a linker (L2) capable of joining the N-terminus to the
 382 C-terminus and having new C- and N-termini at amino acids:
 383

52-53	108-109
53-54	109-110
54-55	110-111
55-56	111-112
56-57	112-113
57-58	113-114
58-59	114-115
59-60	115-116
78-79	116-117
79-80	117-118
80-81	118-119
81-82	119-120
82-83	120-121
83-84	121-122
84-85	122-123
85-86	123-124
86-87	124-125
87-88	125-126
88-89	126-127

	or 127-128 respectively;
--	-----------------------------

384

385

386 (IV) A polypeptide comprising; a modified human IL-3
387 amino acid sequence of the formula:

388

389

390 Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn

391 1 5 10 15

392

393 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

394 20 25 30

395

396 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa

397 35 40 45

398

399 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

400 50 55 60

401

402 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

403 65 70 75

404

405 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

406 80 85 90

407

408 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

409 95 100 105

410

411 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

412 110 115 120

413

414 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe

415 125 130 (SEQ ID NO:2)

416

417 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
418 Arg;
419 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
420 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
421 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
422 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
423 Asn, Thr, Ser or Val;
424 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
425 Gln, Leu, Val or Gly;
426 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
427 Leu, Ser, or Arg;
428 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
429 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
430 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
431 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
432 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
433 Trp;
434 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
435 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
436 or Lys;
437 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
438 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
439 Glu;
440 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
441 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
442 Arg, Ala, Phe, Ile or Met;
443 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
444 Xaa at position 36 is Asp, Leu, or Val;
445 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
446 Xaa at position 38 is Asn, or Ala;
447 Xaa at position 40 is Leu, Trp, or Arg;
448 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
449 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
450 Val, Glu, Phe, Tyr, Ile, Met or Ala;
451 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
452 Gln, Arg, Thr, Gly or Ser;

453 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
454 Glu, Asn, Gln, Ala or Pro;
455 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
456 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
457 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
458 Lys, His, Ala, Tyr, Ile, Val or Gly;
459 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
460 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
461 Lys, Thr, Ala, Met, Val or Asn;
462 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
463 Asp;
464 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
465 Ala, Ile, Val, His, Phe, Met or Gln;
466 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
467 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
468 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
469 or Met;
470 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
471 Lys, His, Ala or Leu;
472 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
473 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
474 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
475 Xaa at position 57 is Asn or Gly;
476 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
477 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
478 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
479 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
480 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
481 Ile;
482 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
483 Val;
484 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
485 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
486 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
487 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
488 or His;

489 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
490 His;
491 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
492 or Leu;
493 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
494 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
495 Trp, or Asn;
496 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
497 Asp;
498 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
499 Arg;
500 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
501 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
502 Gln, or Leu;
503 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
504 or Asp;
505 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
506 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
507 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
508 Asp;
509 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
510 Arg;
511 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
512 Lys;
513 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
514 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
515 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
516 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
517 Xaa at position 85 is Leu, Asn, Val, or Gln;
518 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
519 Xaa at position 87 is Leu, Ser, Trp, or Gly;
520 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
521 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
522 or Ser;
523 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
524 Met;

525 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
526 His;
527 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
528 Ile or Leu;
529 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
530 Arg;
531 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
532 His, Ala, or Pro;
533 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
534 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
535 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
536 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
537 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
538 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
539 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
540 Gly, Ser, Phe, or His;
541 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
542 or Pro;
543 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
544 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
545 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
546 Xaa at position 103 is Asp, or Ser;
547 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
548 Gln, Lys, Ala, Phe, or Gly;
549 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
550 Leu, Lys, Ile, Asp, or His;
551 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
552 Pro;
553 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
554 Ser, Ala or Pro;
555 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
556 Gly;
557 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
558 Glu, Ser, or Trp;
559 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;

560 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
561 Phe;
562 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
563 Lys, Leu, Ile, Val or Asn;
564 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
565 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
566 Trp, or Met;
567 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
568 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
569 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
570 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
571 Tyr;
572 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
573 Arg;
574 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
575 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
576 Gly;
577 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
578 Ile, Tyr, or Cys;
579 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
580 Leu,
581
582 wherein from 1 to 14 amino acids can optionally be deleted
583 from the N-terminus and/or from 1 to 15 amino acids can
584 optionally be deleted from the C-terminus of said modified
585 human IL-3 amino acid sequence; and wherein from 1 to 44 of
586 the amino acids designated by Xaa are different from the
587 corresponding amino acids of native (1-133) human interleukin-
588 3, and
589
590 (V) a colony stimulating factor;
591
592 and wherein L₁ is a linker capable of linking R₁ to R₂
593
594 with the proviso that at least R₁ or R₂ is selected from
595 the polypeptide of formula (I) , (II), or (III); and

596

597 said hematopoietic protein can optionally be immediately
598 preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻²,
599 alanine⁻¹).

1 4. The hematopoietic protein as recited in claim 1
2 wherein the polypeptide of (IV) is selected from the from the
3 group consisting of:

4

5 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

6

7 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu

8

9 Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu

10

11 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly

12

13 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala

14

15 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp

16

17 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu

18

19 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:225);

20

21

22 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

23

24 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu

25

26 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu

27

28 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly

29

30 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala

31

32 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp

33

34 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu

35

36 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:226);

37

38

39 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

40

41 Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
42
43 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
44
45 Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
46
47 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
48
49 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
50
51 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
52
53 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:227); and
54
55
56 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
57 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
58 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
59 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
60 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
61 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
62 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
63 Gln Ala Gln Glu Gln Gln (SEQ ID NO:228).

1 5. The hematopoietic protein as recited in claim 2
2 wherein the polypeptide of (IV) is selected from the from the
3 group consisting of:

4
5 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
6
7 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu
8
9 Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
10
11 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
12
13 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
14
15 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
16
17 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
18
19 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:225);

20
21
22 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
23
24 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
25
26 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
27
28 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
29
30 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
31
32 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
33
34 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
35
36 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:226);
37
38
39 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
40
41 Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
42
43 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
44
45 Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
46
47 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
48
49 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
50
51 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
52
53 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:227); and
54
55 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
56 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
57 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
58 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
59 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
60 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
61 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
62 Gln Ala Gln Glu Gln Gln (SEQ ID NO:228).

1 6. The hematopoietic protein as recited in claim 3
2 wherein the polypeptide of (IV) is selected from the from the
3 group consisting of:

4
5 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
6
7 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu
8
9 Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
10
11 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
12
13 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
14
15 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
16
17 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
18
19 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:225);
20

21
22 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
23
24 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
25
26 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
27
28 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
29
30 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
31
32 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
33
34 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
35
36 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:226);
37

38
39 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
40
41 Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
42
43 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
44
45 Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
46

47 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
 48
 49 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
 50
 51 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
 52
 53 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:227); and
 54
 55 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 56 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 57 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 58 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 59 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 60 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 61 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 62 Gln Ala Gln Glu Gln Gln (SEQ ID NO:228).

1 7. A hematopoietic protein comprising; an amino acid sequence
 2 of the formula:

3
 4 $R_1-L_1-R_2, R_2-L_1-R_1, R_1-R_2, \text{ or } R_2-R_1$

5
 6 wherein R_1 is a polypeptide comprising; a modified human
 7 G-CSF amino acid sequence of the formula:

8
 9 1 10
 10 Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa
 11
 12 20
 13 Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly
 14
 15 30 40
 16 Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa
 17
 18 50
 19 Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp
 20
 21 60 70
 22 Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly
 23
 24 80
 25 Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu

```

46
47 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
48 Xaa at position 2 is Pro or Leu;
49 Xaa at position 3 is Leu, Arg, Tyr or Ser;
50 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
51 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
52 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or Arg;
53 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
54 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
55 Xaa at position 24 is Ile, Pro, Tyr or Leu;
56 Xaa at position 27 is Asp, or Gly;
57 Xaa at position 30 is Ala, Ile, Leu or Gly;
58 Xaa at position 34 is Lys or Ser;
59 Xaa at position 36 is Cys or Ser;
60 Xaa at position 42 is Cys or Ser;
61 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
62 Arg, Cys, or Leu;
63 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
64 Trp, Gln, or Thr;
65 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
66 Xaa at position 47 is Leu or Thr;
67 Xaa at position 49 is Leu, Phe, Arg or Ser;
68 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
69 Xaa at position 54 is Leu or His;
70 Xaa at position 64 is Cys or Ser;
71 Xaa at position 67 is Gln, Lys, Leu or Cys;
72 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;

```

73 Xaa at position 74 is Cys or Ser;
74 Xaa at position 104 is Asp, Gly or Val;
75 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
76 Gly;
77 Xaa at position 115 is Thr, His, Leu or Ala;
78 Xaa at position 120 is Gln, Gly, Arg, Lys or His
79 Xaa at position 123 is Glu, Arg, Phe or Thr
80 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
81 Glu;
82 Xaa at position 146 is Arg or Gln;
83 Xaa at position 147 is Arg or Gln;
84 Xaa at position 156 is His, Gly or Ser;
85 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
86 Xaa at position 162 is Glu, Leu, Gly or Trp;
87 Xaa at position 163 is Val, Gly, Arg or Ala;
88 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
89 Xaa at position 170 is His, Arg or Ser,
90
91 wherein optionally 1-11 amino acids from the N-terminus and 1-
92 5 from the C-terminus can be deleted from said modified human
93 G-CSF amino acid sequence; and
94
95 wherein the N-terminus is joined to the C-terminus directly or
96 through a linker capable of joining the N-terminus to the C-
97 terminus and having new C- and N-termini at amino acids:
98
99
100 38-39 62-63 123-124
101 39-40 63-64 124-125
102 40-41 64-65 125-126
103 41-42 65-66 126-127
104 42-43 66-67 128-129
105 43-44 67-68 128-129
106 45-46 68-69 129-130
107 48-49 69-70 130-131
108 49-50 70-71 131-132
109 52-53 71-72 132-133
110 53-54 91-92 133-134
111 54-55 92-93 134-135
112 55-56 93-94 135-136
113 56-57 94-95 136-137
114 57-58 95-96 137-138
115 58-59 96-97 138-139
116 59-60 97-98 139-140
117 60-61 98-99 140-141
118 61-62 99-100 141-142

or 142-143
respectively,

wherein R₂ is a polypeptide comprising; a modified human
IL-3 amino acid sequence of the formula:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn
1				5					10					15

Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				20					25					30

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				35					40					45

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				50					55					60

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				65					70					75

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				80					85					90

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				95					100					105

Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				110					115					120

Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe		
			125						130	(SEQ ID NO:2)				

wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
Arg;

155 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
156 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
157 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
158 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
159 Asn, Thr, Ser or Val;
160 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
161 Gln, Leu, Val or Gly;
162 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
163 Leu, Ser, or Arg;
164 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
165 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
166 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
167 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
168 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
169 Trp;
170 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
171 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
172 or Lys;
173 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
174 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
175 Glu;
176 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
177 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
178 Arg, Ala, Phe, Ile or Met;
179 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
180 Xaa at position 36 is Asp, Leu, or Val;
181 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
182 Xaa at position 38 is Asn, or Ala;
183 Xaa at position 40 is Leu, Trp, or Arg;
184 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
185 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
186 Val, Glu, Phe, Tyr, Ile, Met or Ala;
187 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
188 Gln, Arg, Thr, Gly or Ser;
189 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
190 Glu, Asn, Gln, Ala or Pro;

191 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
192 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
193 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
194 Lys, His, Ala, Tyr, Ile, Val or Gly;
195 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
196 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
197 Lys, Thr, Ala, Met, Val or Asn;
198 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
199 Asp;
200 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
201 Ala, Ile, Val, His, Phe, Met or Gln;
202 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
203 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
204 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
205 or Met;
206 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
207 Lys, His, Ala or Leu;
208 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
209 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
210 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
211 Xaa at position 57 is Asn or Gly;
212 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
213 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
214 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
215 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
216 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
217 Ile;
218 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
219 Val;
220 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
221 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
222 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
223 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
224 or His;
225 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
226 His;

227 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
228 or Leu;
229 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
230 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
231 Trp, or Asn;
232 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
233 Asp;
234 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
235 Arg;
236 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
237 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
238 Gln, or Leu;
239 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
240 or Asp;
241 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
242 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
243 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
244 Asp;
245 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
246 Arg;
247 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
248 Lys;
249 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
250 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
251 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
252 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
253 Xaa at position 85 is Leu, Asn, Val, or Gln;
254 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
255 Xaa at position 87 is Leu, Ser, Trp, or Gly;
256 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
257 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
258 or Ser;
259 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
260 Met;
261 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
262 His;

263 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
264 Ile or Leu;
265 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
266 Arg;
267 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
268 His, Ala, or Pro;
269 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
270 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
271 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
272 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
273 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
274 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
275 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
276 Gly, Ser, Phe, or His;
277 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
278 or Pro;
279 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
280 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
281 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
282 Xaa at position 103 is Asp, or Ser;
283 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
284 Gln, Lys, Ala, Phe, or Gly;
285 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
286 Leu, Lys, Ile, Asp, or His;
287 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
288 Pro;
289 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
290 Ser, Ala or Pro;
291 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
292 Gly;
293 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
294 Glu, Ser, or Trp;
295 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
296 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
297 Phe;
298 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,

299 Lys, Leu, Ile, Val or Asn;
 300 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
 301 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
 302 Trp, or Met;
 303 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
 304 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
 305 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
 306 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
 307 Tyr;
 308 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
 309 Arg;
 310 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
 311 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
 312 Gly;
 313 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
 314 Ile, Tyr, or Cys;
 315 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
 316 Leu,
 317
 318 wherein from 1 to 14 amino acids can optionally be deleted
 319 from the N-terminus and/or from 1 to 15 amino acids can
 320 optionally be deleted from the C-terminus of said modified
 321 human interleukin-3 amino acid sequence; and wherein from 0 to
 322 44 of the amino acids designated by Xaa are different from the
 323 corresponding amino acids of native (1-133) human interleukin-
 324 3 and
 325
 326 wherein the N-terminus is joined to the C-terminus directly or
 327 through a linker (L₂) capable of joining the N-terminus to the
 328 C-terminus and having new C- and N-termini at amino acids:
 329

26-27	49-50	83-84
27-28	50-51	84-85
28-29	51-52	85-86
29-30	52-53	86-87
30-31	53-54	87-88
31-32	54-55	88-89

32-33	64-65	89-90
33-34	65-66	90-91
34-35	66-67	91-92
35-36	67-68	92-93
36-37	68-69	97-98
37-38	69-70	98-99
38-39	70-71	99-100
39-40	71-72	100-101
40-41	72-73	101-102
41-42	82-83	102-103
		or 103-104 respectively;

330

331

332 wherein L₁ is a linker capable of linking R₁ to R₂ and

333

334 said hematopoietic protein can optionally be immediately
335 preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻²,
336 alanine⁻¹).

1 8. A hematopoietic protein comprising; an amino acid sequence
2 of the formula:

3

4 R₁-L₁-R₂, R₂-L₁-R₁, R₁-R₂, or R₂-R₁

5

6 wherein R₁ is a polypeptide comprising; a modified human
7 G-CSF amino acid sequence of the formula:

8

9 1 10
10 Xaa Xaa Xaa Gly Pro Ala Ser Ser Leu Pro Gln Ser Xaa

11

12 20
13 Leu Leu Xaa Xaa Xaa Glu Gln Val Xaa Lys Xaa Gln Gly Xaa Gly

14

15 30 40
16 Ala Xaa Leu Gln Glu Xaa Leu Xaa Ala Thr Tyr Lys Leu Xaa Xaa

17

18 50
19 Xaa Glu Xaa Xaa Val Xaa Xaa Gly His Ser Xaa Gly Ile Pro Trp

20

21 60 70
22 Ala Pro Leu Ser Ser Xaa Pro Ser Xaa Ala Leu Xaa Leu Ala Gly

23
24
25 Xaa Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
26
27 90 100
28 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
29
30 110
31 Xaa Thr Leu Gln Xaa Asp Val Ala Asp Phe Ala Xaa Thr Ile Trp
32
33 120 130
34 Gln Gln Met Glu Xaa Xaa Gly Met Ala Pro Ala Leu Gln Pro Thr
35
36 140
37 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Xaa Gln Xaa Xaa Ala
38
39 150 160
40 Gly Gly Val Leu Val Ala Ser Xaa Leu Gln Xaa Phe Leu Xaa Xaa
41
42 170
43 Ser Tyr Arg Val Leu Xaa Xaa Leu Ala Gln Pro (SEQ ID NO:1)
44
45 wherein
46
47 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
48 Xaa at position 2 is Pro or Leu;
49 Xaa at position 3 is Leu, Arg, Tyr or Ser;
50 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
51 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
52 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or
53 Arg;
54 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
55 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
56 Xaa at position 24 is Ile, Pro, Tyr or Leu;
57 Xaa at position 27 is Asp, or Gly;
58 Xaa at position 30 is Ala, Ile, Leu or Gly;
59 Xaa at position 34 is Lys or Ser;
60 Xaa at position 36 is Cys or Ser;
61 Xaa at position 42 is Cys or Ser;
62 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
63 Arg, Cys, or Leu;
64 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
65 Trp, Gln, or Thr;
66 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
67 Xaa at position 47 is Leu or Thr;
68 Xaa at position 49 is Leu, Phe, Arg or Ser;
69 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;

70 Xaa at position 54 is Leu or His;
71 Xaa at position 64 is Cys or Ser;
72 Xaa at position 67 is Gln, Lys, Leu or Cys;
73 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
74 Xaa at position 74 is Cys or Ser;
75 Xaa at position 104 is Asp, Gly or Val;
76 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
77 Gly;
78 Xaa at position 115 is Thr, His, Leu or Ala;
79 Xaa at position 120 is Gln, Gly, Arg, Lys or His
80 Xaa at position 123 is Glu, Arg, Phe or Thr
81 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
82 Glu;
83 Xaa at position 146 is Arg or Gln;
84 Xaa at position 147 is Arg or Gln;
85 Xaa at position 156 is His, Gly or Ser;
86 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
87 Xaa at position 162 is Glu, Leu, Gly or Trp;
88 Xaa at position 163 is Val, Gly, Arg or Ala;
89 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
90 Xaa at position 170 is His, Arg or Ser;
91
92 wherein optionally 1-11 amino acids from the N-terminus and 1-
93 5 from the C-terminus can be deleted from said modified human
94 G-CSF amino acid sequence and
95
96 wherein the N-terminus is joined to the C-terminus directly or
97 through a linker capable of joining the N-terminus to the C-
98 terminus and having new C- and N-termini at amino acids:
99
100
101 38-39 62-63 123-124
102 39-40 63-64 124-125
103 40-41 64-65 125-126
104 41-42 65-66 126-127
105 42-43 66-67 128-129
106 43-44 67-68 128-129
107 45-46 68-69 129-130
108 48-49 69-70 130-131
109 49-50 70-71 131-132
110 52-53 71-72 132-133
111 53-54 91-92 133-134
112 54-55 92-93 134-135
113 55-56 93-94 135-136
114 56-57 94-95 136-137
115 57-58 95-96 137-138

116 58-59 96-97 138-139
 117 59-60 97-98 139-140
 118 60-61 98-99 140-141
 119 61-62 99-100 141-142
 120 or 142-143
 121 respectively; and
 122

123 R₂ is a polypeptide comprising a modified human IL-3
 124 amino acid sequence of the formula:
 125

126	Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn
127	1				5					10					15
128															
129	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
130					20					25					30
131															
132	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
133					35					40					45
134															
135	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
136					50					55					60
137															
138	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
139					65					70					75
140															
141	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
142					80					85					90
143															
144	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					95					100					105
146															
147	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
148					110					115					120
149															
150	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu	Ser	Leu	Ala	Ile	Phe		
151				125						130	(SEQ ID NO:2)				
152															

153 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
154 Arg;
155 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;
156 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
157 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
158 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
159 Asn, Thr, Ser or Val;
160 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
161 Gln, Leu, Val or Gly;
162 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
163 Leu, Ser, or Arg;
164 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
165 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
166 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
167 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
168 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
169 Trp;
170 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
171 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
172 or Lys;
173 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
174 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
175 Glu;
176 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
177 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
178 Arg, Ala, Phe, Ile or Met;
179 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
180 Xaa at position 36 is Asp, Leu, or Val;
181 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
182 Xaa at position 38 is Asn, or Ala;
183 Xaa at position 40 is Leu, Trp, or Arg;
184 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
185 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
186 Val, Glu, Phe, Tyr, Ile, Met or Ala;
187 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
188 Gln, Arg, Thr, Gly or Ser;

189 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
190 Glu, Asn, Gln, Ala or Pro;
191 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,
192 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
193 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
194 Lys, His, Ala, Tyr, Ile, Val or Gly;
195 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
196 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
197 Lys, Thr, Ala, Met, Val or Asn;
198 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
199 Asp;
200 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
201 Ala, Ile, Val, His, Phe, Met or Gln;
202 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
203 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
204 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
205 or Met;
206 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
207 Lys, His, Ala or Leu;
208 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
209 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
210 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
211 Xaa at position 57 is Asn or Gly;
212 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
213 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
214 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
215 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
216 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
217 Ile;
218 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
219 Val;
220 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
221 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
222 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
223 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
224 or His;

225 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
226 His;
227 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
228 or Leu;
229 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
230 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
231 Trp, or Asn;
232 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
233 Asp;
234 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
235 Arg;
236 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
237 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
238 Gln, or Leu;
239 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
240 or Asp;
241 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
242 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
243 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
244 Asp;
245 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
246 Arg;
247 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
248 Lys;
249 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
250 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
251 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
252 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
253 Xaa at position 85 is Leu, Asn, Val, or Gln;
254 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
255 Xaa at position 87 is Leu, Ser, Trp, or Gly;
256 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
257 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
258 or Ser;
259 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
260 Met;

261 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
262 His;
263 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
264 Ile or Leu;
265 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
266 Arg;
267 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
268 His,
269 Ala, or Pro;
270 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
271 Asn,
272 Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
273 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
274 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
275 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
276 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
277 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
278 Gly, Ser, Phe, or His;
279 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
280 or Pro;
281 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
282 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
283 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
284 Xaa at position 103 is Asp, or Ser;
285 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
286 Gln, Lys, Ala, Phe, or Gly;
287 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
288 Leu, Lys, Ile, Asp, or His;
289 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
290 Pro;
291 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
292 Ser, Ala or Pro;
293 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
294 Gly;
295 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
296 Glu, Ser, or Trp;

297 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
298 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
299 Phe;
300 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,
301 Lys, Leu, Ile, Val or Asn;
302 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
303 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
304 Trp, or Met;
305 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
306 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
307 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
308 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
309 Tyr;
310 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
311 Arg;
312 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
313 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
314 Gly;
315 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
316 Ile, Tyr, or Cys;
317 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
318 Leu,
319
320 wherein from 1 to 14 amino acids can optionally be deleted
321 from the N-terminus and/or from 1 to 15 amino acids can
322 optionally be deleted from the C-terminus; and wherein from 1
323 to 44 of the amino acids designated by Xaa are different from
324 the corresponding amino acids of native (1-133) human
325 interleukin-3 and
326
327 L₁ is a linker capable of linking R₁ to R₂ and
328
329 additionally said hematopoietic protein can be
330 immediately preceded by (methionine⁻¹), (alanine⁻¹) or
331 (methionine⁻², alanine⁻¹).

46
47 Xaa at position 1 is Thr, Ser, Arg, Tyr or Gly;
48 Xaa at position 2 is Pro or Leu;
49 Xaa at position 3 is Leu, Arg, Tyr or Ser;
50 Xaa at position 13 is Phe, Ser, His, Thr or Pro;
51 Xaa at position 16 is Lys, Pro, Ser, Thr or His;
52 Xaa at position 17 is Cys, Ser, Gly, Ala, Ile, Tyr or
53 Arg;
54 Xaa at position 18 is Leu, Thr, Pro, His, Ile or Cys;
55 Xaa at position 22 is Arg, Tyr, Ser, Thr or Ala;
56 Xaa at position 24 is Ile, Pro, Tyr or Leu;
57 Xaa at position 27 is Asp, or Gly;
58 Xaa at position 30 is Ala, Ile, Leu or Gly;
59 Xaa at position 34 is Lys or Ser;
60 Xaa at position 36 is Cys or Ser;
61 Xaa at position 42 is Cys or Ser;
62 Xaa at position 43 is His, Thr, Gly, Val, Lys, Trp, Ala,
63 Arg, Cys, or Leu;
64 Xaa at position 44 is Pro, Gly, Arg, Asp, Val, Ala, His,
65 Trp, Gln, or Thr;
66 Xaa at position 46 is Glu, Arg, Phe, Arg, Ile or Ala;
67 Xaa at position 47 is Leu or Thr;
68 Xaa at position 49 is Leu, Phe, Arg or Ser;
69 Xaa at position 50 is Leu, Ile, His, Pro or Tyr;
70 Xaa at position 54 is Leu or His;
71 Xaa at position 64 is Cys or Ser;
72 Xaa at position 67 is Gln, Lys, Leu or Cys;
73 Xaa at position 70 is Gln, Pro, Leu, Arg or Ser;
74 Xaa at position 74 is Cys or Ser;
75 Xaa at position 104 is Asp, Gly or Val;
76 Xaa at position 108 is Leu, Ala, Val, Arg, Trp, Gln or
77 Gly;
78 Xaa at position 115 is Thr, His, Leu or Ala;
79 Xaa at position 120 is Gln, Gly, Arg, Lys or His
80 Xaa at position 123 is Glu, Arg, Phe or Thr
81 Xaa at position 144 is Phe, His, Arg, Pro, Leu, Gln or
82 Glu;
83 Xaa at position 146 is Arg or Gln;
84 Xaa at position 147 is Arg or Gln;
85 Xaa at position 156 is His, Gly or Ser;
86 Xaa at position 159 is Ser, Arg, Thr, Tyr, Val or Gly;
87 Xaa at position 162 is Glu, Leu, Gly or Trp;
88 Xaa at position 163 is Val, Gly, Arg or Ala;
89 Xaa at position 169 is Arg, Ser, Leu, Arg or Cys;
90 Xaa at position 170 is His, Arg or Ser,
91

wherein optionally 1-11 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted from said modified human G-CSF amino acid sequence and

wherein the N-terminus is joined to the C-terminus directly or through a linker capable of joining the N-terminus to the C-terminus and having new C- and N-termini at amino acids:

38-39	62-63	123-124
39-40	63-64	124-125
40-41	64-65	125-126
41-42	65-66	126-127
42-43	66-67	128-129
43-44	67-68	128-129
45-46	68-69	129-130
48-49	69-70	130-131
49-50	70-71	131-132
52-53	71-72	132-133
53-54	91-92	133-134
54-55	92-93	134-135
55-56	93-94	135-136
56-57	94-95	136-137
57-58	95-96	137-138
58-59	96-97	138-139
59-60	97-98	139-140
60-61	98-99	140-141
61-62	99-100	141-142
		or 142-143
		respectively; and

R₂ is a polypeptide comprising a modified human c-mpl ligand amino acid sequence of the formula:

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1 5 10 15
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
20 25 30 35
ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
40 45 50 55
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
60 65 70 75

137
 138 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
 139 80 85 90 95
 140
 141 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
 142 100 105 110
 143
 144 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 145 115 120 125 130
 146
 147 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
 148 135 140 145 150
 149
 150 Arg (SEQ ID NO:256)
 151
 152 wherein
 153
 154 Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro,
 155 Phe, Trp, or Met;
 156 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 157 Ile, Trp, or Met;
 158 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 159 Ile, Trp, or Met;
 160 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 161 Asn, and
 162
 163 wherein the N-terminus is joined to the C-terminus directly or
 164 through a linker (L2) capable of joining the N-terminus to the
 165 C-terminus and having new C- and N-termini at amino acids:
 166

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119

40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127
50-51	88-89	or 127-128;

wherein L₁ is a linker capable of linking R₁ to R₂ and

additionally said hematopoietic protein can be immediately preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻², alanine⁻¹).

10. A hematopoietic protein comprising; an amino acid sequence of the formula:

R₁-L₁-R₂, R₂-L₁-R₁, R₁-R₂, or R₂-R₁

wherein R₁ is a polypeptide comprising a modified human c-mpl ligand amino acid sequence of the formula:

```

SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
1      5      10      15
HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
20     25     30     35
ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
40     45     50     55
ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
60     65     70     75
AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
80     85     90     95
GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
100    105    110
XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis

```

28 115 120 125 130
 29
 30 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal
 31 135 140 145 150
 32
 33 Arg (SEQ ID NO:256)
 34 153
 35
 36 wherein
 37
 38 Xaa at position 112 is deleted or Leu, Ala, Val, Ile, Pro,
 39 Phe, Trp, or Met;
 40 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 41 Ile, Trp, or Met;
 42 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 43 Ile, Trp, or Met;
 44 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 45 Asn, and
 46
 47 wherein the N-terminus is joined to the C-terminus directly or
 48 through a linker (L2) capable of joining the N-terminus to the
 49 C-terminus and having new C- and N-termini at amino acids:
 50

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126

48-49	87-88	126-127
50-51	88-89	or 127-128;

51 wherein R₂ is a polypeptide comprising a modified human
52 IL-3 amino acid sequence of the formula:
53
54
55 Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
56 1 5 10 15
57
58 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
59 20 25 30
60
61 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa
62 35 40 45
63
64 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 50 55 60
66
67 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
68 65 70 75
69
70 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
71 80 85 90
72
73 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
74 95 100 105
75
76 Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
77 110 115 120
78
79 Xaa Xaa Xaa Gln Gln Thr Thr Leu Ser Leu Ala Ile Phe
80 125 130 (SEQ ID NO:2)
81
82 wherein Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or
83 Arg;
84 Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln;

85 Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys;
86 Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala;
87 Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln,
88 Asn, Thr, Ser or Val;
89 Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn,
90 Gln, Leu, Val or Gly;
91 Xaa at position 23 is Ile, Val, Ala, Gly, Trp, Lys, Phe,
92 Leu, Ser, or Arg;
93 Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu;
94 Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala;
95 Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp;
96 Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala;
97 Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val or
98 Trp;
99 Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val;
100 Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu,
101 or Lys;
102 Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln;
103 Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or
104 Glu;
105 Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu;
106 Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr,
107 Arg, Ala, Phe, Ile or Met;
108 Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val;
109 Xaa at position 36 is Asp, Leu, or Val;
110 Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile;
111 Xaa at position 38 is Asn, or Ala;
112 Xaa at position 40 is Leu, Trp, or Arg;
113 Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro;
114 Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu,
115 Val, Glu, Phe, Tyr, Ile, Met or Ala;
116 Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys,
117 Gln, Arg, Thr, Gly or Ser;
118 Xaa at position 44 is Asp, Ser, Leu, Arg, Lys, Thr, Met, Trp,
119 Glu, Asn, Gln, Ala or Pro;
120 Xaa at position 45 is Gln, Pro, Phe, Val, Met, Leu, Thr, Lys,

121 Trp, Asp, Asn, Arg, Ser, Ala, Ile, Glu or His;
122 Xaa at position 46 is Asp, Phe, Ser, Thr, Cys, Glu, Asn, Gln,
123 Lys, His, Ala, Tyr, Ile, Val or Gly;
124 Xaa at position 47 is Ile, Gly, Val, Ser, Arg, Pro, or His;
125 Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu,
126 Lys, Thr, Ala, Met, Val or Asn;
127 Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or
128 Asp;
129 Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser,
130 Ala, Ile, Val, His, Phe, Met or Gln;
131 Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His;
132 Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr;
133 Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser,
134 or Met;
135 Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn,
136 Lys, His, Ala or Leu;
137 Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly;
138 Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His,
139 Thr, Ala, Tyr, Phe, Leu, Val or Lys;
140 Xaa at position 57 is Asn or Gly;
141 Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys;
142 Xaa at position 59 is Glu Tyr, His, Leu, Pro, or Arg;
143 Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr;
144 Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser;
145 Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or
146 Ile;
147 Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or
148 Val;
149 Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys;
150 Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser;
151 Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser;
152 Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro,
153 or His;
154 Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or
155 His;

156 Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly,
157 or Leu;
158 Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala;
159 Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln,
160 Trp, or Asn;
161 Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or
162 Asp;
163 Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or
164 Arg;
165 Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, Ala;
166 Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser,
167 Gln, or Leu;
168 Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly,
169 or Asp;
170 Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu;
171 Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg;
172 Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or
173 Asp;
174 Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or
175 Arg;
176 Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or
177 Lys;
178 Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn,
179 His, Thr, Ser, Ala, Tyr, Phe, Ile, Met or Val;
180 Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met;
181 Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val;
182 Xaa at position 85 is Leu, Asn, Val, or Gln;
183 Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys;
184 Xaa at position 87 is Leu, Ser, Trp, or Gly;
185 Xaa at position 88 is Ala, Lys, Arg, Val, or Trp;
186 Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn,
187 or Ser;
188 Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or
189 Met;
190 Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or
191 His;

192 Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly,
193 Ile or Leu;
194 Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or
195 Arg;
196 Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys,
197 His, Ala, or Pro;
198 Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr,
199 Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr;
200 Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr;
201 Xaa at position 97 is Ile, Val, Lys, Ala, or Asn;
202 Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr,
203 Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr or Pro;
204 Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln,
205 Gly, Ser, Phe, or His;
206 Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln,
207 or Pro;
208 Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val,
209 Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln;
210 Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro;
211 Xaa at position 103 is Asp, or Ser;
212 Xaa at position 104 is Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu,
213 Gln, Lys, Ala, Phe, or Gly;
214 Xaa at position 105 is Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr,
215 Leu, Lys, Ile, Asp, or His;
216 Xaa at position 106 is Glu, Ser, Ala, Lys, Thr, Ile, Gly, or
217 Pro;
218 Xaa at position 108 is Arg, Lys, Asp, Leu, Thr, Ile, Gln, His,
219 Ser, Ala or Pro;
220 Xaa at position 109 is Arg, Thr, Pro, Glu, Tyr, Leu, Ser, or
221 Gly;
222 Xaa at position 110 is Lys, Ala, Asn, Thr, Leu, Arg, Gln, His,
223 Glu, Ser, or Trp;
224 Xaa at position 111 is Leu, Ile, Arg, Asp, or Met;
225 Xaa at position 112 is Thr, Val, Gln, Tyr, Glu, His, Ser, or
226 Phe;
227 Xaa at position 113 is Phe, Ser, Cys, His, Gly, Trp, Tyr, Asp,

228 Lys, Leu, Ile, Val or Asn;
229 Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu;
230 Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr,
231 Trp, or Met;
232 Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu,
233 Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile;
234 Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro;
235 Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or
236 Tyr;
237 Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or
238 Arg;
239 Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln;
240 Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or
241 Gly;
242 Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His,
243 Ile, Tyr, or Cys;
244 Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or
245 Leu,
246
247 wherein from 1 to 14 amino acids can optionally be deleted
248 from the N-terminus and/or from 1 to 15 amino acids can
249 optionally be deleted from the C-terminus of said modified
250 human interleukin-3 amino acid sequence; and wherein from 1 to
251 44 of the amino acids designated by Xaa are different from the
252 corresponding amino acids of native (1-133) human interleukin-
253 3;
254
255 wherein L₁ is a linker capable of linking R₁ to R₂; and
256
257 said hematopoietic protein can optionally be immediately
258 preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻²,
259 alanine⁻¹).

1 11. The hematopoietic protein of claim 8 or 10 wherein R₂ is
2 selected from the group consisting of:
3

4 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
5
6 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu
7
8 Asp Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
9
10 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
11
12 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
13
14 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
15
16 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
17
18 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:225);
19
20
21 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
22
23 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu
24
25 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu
26
27 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly
28
29 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
30
31 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
32
33 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
34
35 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:226);
36
37
38 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
39
40 Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu
41
42 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu
43
44 Leu Ala Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
45
46 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
47
48 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
49
50 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu

51
 52 Glu Gln Ala Gln Glu Gln Gln (SEQ ID NO:227); and
 53
 54 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 55 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 56 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 57 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 58 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 59 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 60 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 61 Gln Ala Gln Glu Gln Gln (SEQ ID NO:228).

1 12. A hematopoietic protein comprising; an amino acid sequence
 2 of the formula:

3
 4 $R_1-L_1-R_2$, $R_2-L_1-R_1$, R_1-R_2 , or R_2-R_1

5
 6 wherein R_1 is a polypeptide comprising; a modified human
 7 c-mpl ligand amino acid sequence of the formula:

8
 9 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
 10 1 5 10 15
 11
 12 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrPro
 13 20 25 30 35
 14
 15 ValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGlu
 16 40 45 50 55
 17
 18 ThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
 19 60 65 70 75
 20
 21 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
 22 80 85 90 95
 23
 24 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnXaaXaaXaa
 25 100 105 110
 26
 27 XaaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 28 115 120 125 130
 29
 30 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysVal

31 135 140 145 150
 32
 33 Arg (SEQ ID NO:256)
 34 153
 35
 36 wherein
 37
 38 Xaa at position 112 is deleted or Leu, Ala, Val, Ile,
 39 Pro, Phe, Trp, or Met;
 40 Xaa at position 113 is deleted or Pro, Phe, Ala, Val, Leu,
 41 Ile, Trp, or Met;
 42 Xaa at position 114 is deleted or Pro, Phe, Ala, Val, Leu,
 43 Ile, Trp, or Met;
 44 Xaa at position 115 is deleted or Gln, Gly, Ser, Thr, Tyr, or
 45 Asn; and
 46
 47 wherein the N-terminus is joined to the C-terminus directly or
 48 through a linker (L2) capable of joining the N-terminus to the
 49 C-terminus and having new C- and N-termini at amino acids:
 50

26-27	51-52	108-109
27-28	52-53	109-110
28-29	53-54	110-111
29-30	54-55	111-112
30-31	55-56	112-113
32-33	56-57	113-114
33-34	57-58	114-115
34-35	58-59	115-116
36-37	59-60	116-117
37-38	78-79	117-118
38-39	79-80	118-119
40-41	80-81	119-120
41-42	81-82	120-121
42-43	82-83	121-122
43-44	83-84	122-123
44-45	84-85	123-124
46-47	85-86	124-125
47-48	86-87	125-126
48-49	87-88	126-127

50-51	88-89	or 127-128 respectively;
-------	-------	-----------------------------

51
52 wherein R₂ is G-CSF or G-CSF Ser¹⁷
53
54 wherein L₁ is a linker capable of linking R₁ to R₂; and
55
56 said hematopoietic protein can optionally be immediately
57 preceded by (methionine⁻¹), (alanine⁻¹) or (methionine⁻²,
58 alanine⁻¹).

1 13. The hematopoietic protein as recited in claim 1, 2,
2 3, 4, 5, 6, 7, 8, 9, 10 or 12 wherein said linker (L₂) is
3 selected from the group consisting of;
4 GlyGlyGlySer (SEQ ID NO:12);
5 GlyGlyGlySerGlyGlyGlySer (SEQ ID NO:242);
6 GlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
7 (SEQ ID NO:243);
8 SerGlyGlySerGlyGlySer (SEQ ID NO:244);
9 GluPheGlyAsnMetAla (SEQ ID NO:245);
10 GluPheGlyGlyAsnMetAla (SEQ ID NO:246);
11 GluPheGlyGlyAsnGlyGlyAsnMetAla (SEQ ID NO:247); and
12 GlyGlySerAspMetAlaGly (SEQ ID NO:248).

1 14. The hematopoietic protein as recited in claim 11
2 wherein said linker (L₂) is selected from the group consisting
3 of:
4 GlyGlyGlySer (SEQ ID NO:12);
5 GlyGlyGlySerGlyGlyGlySer (SEQ ID NO:242);
6 GlyGlyGlySerGlyGlyGlySerGlyGlyGlySer
7 (SEQ ID NO:243);
8 SerGlyGlySerGlyGlySer (SEQ ID NO:244);
9 GluPheGlyAsnMetAla (SEQ ID NO:245);
10 GluPheGlyGlyAsnMetAla (SEQ ID NO:246);
11 GluPheGlyGlyAsnGlyGlyAsnMetAla (SEQ ID NO:247); and
12 GlyGlySerAspMetAlaGly (SEQ ID NO:248).

15. The hematopoietic protein as recited in claim 1
wherein said protein is selected from the group consisting of:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
Ala Thr (SEQ ID NO:166);

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val

48 Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
49 Ala Thr (SEQ ID NO:167);
50
51
52 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
53 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
54 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
55 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
56 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
57 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
58 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
59 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
60 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Pro Glu Leu Gly
61 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
62 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
63 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
64 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
65 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
66 Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
67 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
68 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
69 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
70 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
71 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
72 Ile Ser (SEQ ID NO:168);
73
74
75 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
76 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
77 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
78 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
79 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
80 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
81 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
82 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
83 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
84 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
85 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
86 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
87 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
88 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
89 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
90 Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
91 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
92 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
93 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
94 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His

95 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
96 Ile Ser (SEQ ID NO:169);
97
98
99 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
100 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
101 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
102 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
103 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
104 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
105 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
106 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
107 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Met Ala Pro Ala
108 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
109 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
110 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
111 Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
112 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
113 Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
114 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
115 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
116 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
117 Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
118 Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
119 Leu Gly (SEQ ID NO:170);
120
121
122 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
123 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
124 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
125 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
126 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
127 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
128 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
129 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
130 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
131 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
132 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
133 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
134 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
135 Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu
136 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
137 Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
138 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
139 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
140 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
141 Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu

142 Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
143 Leu Gly (SEQ ID NO:171);
144
145
146 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
147 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
148 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
149 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
150 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
151 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
152 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
153 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
154 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
155 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
156 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
157 Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
158 Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
159 Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
160 Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
161 Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
162 Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
163 Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
164 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
165 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
166 Gln Pro (SEQ ID NO:172);
167
168
169 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
170 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
171 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
172 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
173 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
174 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
175 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
176 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
177 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
178 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
179 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
180 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
181 Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser
182 Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
183 Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
184 Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
185 Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln
186 Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr
187 Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly
188 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr

189 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
 190 Gln Pro (SEQ ID NO:173);
 191
 192
 193 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 194 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 195 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 196 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 197 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 198 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 199 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 200 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
 201 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
 202 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 203 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
 204 Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
 205 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
 206 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
 207 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 208 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 209 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 210 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
 211 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
 212 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 213 Phe Ala (SEQ ID NO:177);
 214
 215
 216 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 217 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 218 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 219 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 220 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 221 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 222 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 223 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
 224 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
 225 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser Ala Phe Gln
 226 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 227 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser
 228 Gly Gly Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu
 229 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
 230 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
 231 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 232 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 233 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 234 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
 235 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu

236 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
237 Phe Ala (SEQ ID NO:175);
238
239
240 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
241 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
242 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
243 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
244 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
245 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
246 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
247 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
248 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Tyr Lys Leu Cys
249 His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
250 Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
251 Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
252 Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
253 Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
254 Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
255 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
256 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
257 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
258 Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
259 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
260 Lys Leu Cys Ala Thr (SEQ ID NO:176);
261
262
263 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
264 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
265 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
266 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
267 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
268 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
269 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
270 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
271 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
272 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Tyr Lys Leu Cys
273 His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
274 Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
275 Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
276 Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
277 Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
278 Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
279 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
280 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
281 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu
282 Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu

283 Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 284 Lys Leu Cys Ala Thr (SEQ ID NO:177);
 285
 286
 287 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 288 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 289 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 290 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 291 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 292 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 293 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 294 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
 295 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
 296 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro Glu Leu Gly
 297 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr
 298 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu
 299 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln
 300 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
 301 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
 302 Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
 303 Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
 304 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
 305 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
 306 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
 307 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
 308 Leu Glu Gly Ile Ser (SEQ ID NO:179);
 309
 310
 311 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 312 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 313 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 314 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
 315 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
 316 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
 317 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 318 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
 319 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
 320 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Met Ala Pro Ala
 321 Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 322 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
 323 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 324 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 325 Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
 326 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu
 327 Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
 328 Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 329 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln

330 Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
331 Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
332 Met Glu Glu Leu Gly (SEQ ID NO:181);
333
334
335 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
336 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
337 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
338 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
339 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
340 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
341 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
342 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
343 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Thr Gln Gly Ala
344 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
345 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
346 Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
347 Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
348 Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
349 Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
350 Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
351 Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
352 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
353 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
354 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
355 Pro Ala Leu Gln Pro (SEQ ID NO:182);
356
357
358 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
359 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
360 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
361 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
362 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
363 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
364 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
365 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
366 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
367 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala
368 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
369 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg
370 Val Leu Arg His Leu Ala Gln Pro Thr Pro Leu Gly Pro Ala Ser
371 Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
372 Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
373 Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His
374 Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln
375 Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
376 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro

377 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
378 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
379 Pro Ala Leu Gln Pro (SEQ ID NO:183);
380
381
382 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
383 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
384 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
385 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
386 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr
387 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp
388 Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
389 Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro
390 Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Ser Ala Phe Gln
391 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
392 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr
393 Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
394 Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
395 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu
396 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu
397 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
398 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala
399 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu
400 Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met
401 Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala
402 Met Pro Ala Phe Ala (SEQ ID NO:184);
403
404
405 MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
406 ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
407 LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
408 GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
409 SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
410 PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
411 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
412 SerHisLysSerProAsnMetAlaTyrLysLeuCysHisProGluGluLeuValLeuLeu
413 GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
414 LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
415 AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
416 AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
417 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGly
418 ValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHis
419 LeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeu
420 ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAla
421 AlaLeuGlnGluLysLeuCysAlaThr (SEQ ID NO:194);
422
423

424 MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
425 ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
426 LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
427 GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
428 SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
429 PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
430 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
431 SerHisLysSerProAsnMetAlaProGluLeuGlyProThrLeuAspThrLeuGlnLeu
432 AspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaPro
433 AlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAla
434 GlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeu
435 ArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSer
436 SerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp
437 GlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeu
438 ValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGln
439 AlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGly
440 LeuLeuGlnAlaLeuGluGlyIleSer (SEQ ID NO:195);

441
442
443 MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
444 ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
445 LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
446 GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
447 SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
448 PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
449 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
450 SerHisLysSerProAsnMetAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuVal
451 AlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGln
452 ProGlyGlyGlySerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSer
453 PheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGln
454 GluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHis
455 SerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAla
456 GlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu
457 GluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAsp
458 PheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro
459 ThrGlnGlyAlaMetProAlaPheAla (SEQ ID NO:196);

460
461
462 MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
463 ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
464 LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
465 GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
466 SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
467 PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
468 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
469 SerHisLysSerProAsnMetAlaMetAlaProAlaLeuGlnProThrGlnGlyAlaMet
470 ProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeu

471 GlnSerPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnProGlyGlyGly
472 SerAspMetAlaThrProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLys
473 SerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCys
474 AlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSerLeuGlyIle
475 ProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSer
476 GlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer
477 ProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThr
478 IleTrpGlnGlnMetGluGluLeuGly (SEQ ID NO:197);

479
480
481 MetAlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAla
482 ProLeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsn
483 LeuArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSer
484 GlyIleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaPro
485 SerArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThr
486 PheTyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGly
487 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
488 SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
489 GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
490 TyrArgValLeuArgHisLeuAlaGlnProGlyGlyGlySerAspMetAlaThrProLeu
491 GlyProAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLys
492 IleGlnGlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHis
493 ProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer
494 CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPhe
495 LeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyProThrLeu
496 AspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGlu
497 LeuGlyMetAlaProAlaLeuGlnPro (SEQ ID NO:198);

498
499
500 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
501 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
502 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
503 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
504 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
505 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
506 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
507 Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Ser Pro
508 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
509 Ser Lys Glu Ser His Lys Ser Pro Asn Met Gly Pro Thr Cys Leu
510 Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu
511 Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly
512 Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe
513 Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly
514 Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn Met Ala Ser
515 Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
516 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu
517 Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe

518 Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
519 Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala
520 Ala Arg Gly Gln Leu (SEQ ID NO:209);
521
522
523 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
524 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
525 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
526 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
527 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
528 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
529 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
530 Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Ser Pro
531 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
532 Ser Lys Glu Ser His Lys Ser Pro Asn Met Gly Thr Gln Leu Pro
533 Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
534 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
535 Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe Gly Gly Asn
536 Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser
537 Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln
538 Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
539 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr
540 Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly
541 Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser
542 Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala
543 Leu Gln Ser Leu Leu (SEQ ID NO:210);
544
545
546 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
547 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
548 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
549 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
550 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
551 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
552 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
553 Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Ser Pro
554 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
555 Ser Lys Glu Ser His Lys Ser Pro Asn Met Gly Arg Thr Thr Ala
556 His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu
557 Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu
558 Cys Val Arg Glu Phe Gly Gly Asn Met Ala Ser Pro Ala Pro Pro
559 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His
560 Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu
561 Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu
562 Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly
563 Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
564 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly

565 Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr
 566 Gln Leu Pro Pro Gln (SEQ ID NO:211);
 567
 568
 569 Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 570 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu
 571 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
 572 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly
 573 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala
 574 Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp
 575 Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu
 576 Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly Ser Pro
 577 Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro
 578 Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala His Lys Asp Pro
 579 Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val
 580 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu
 581 Phe Gly Gly Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu
 582 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
 583 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
 584 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
 585 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
 586 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
 587 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
 588 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
 589 Gln Gly Arg Thr Thr (SEQ ID NO:212);
 590
 591
 592 Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
 593 Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
 594 Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
 595 Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
 596 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
 597 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 598 Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp Glu Ile Ile
 599 His His Leu Lys Arg Pro Pro Ala Pro Leu Tyr Val Glu Gly Gly
 600 Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
 601 Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
 602 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
 603 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
 604 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
 605 Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
 606 Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
 607 Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
 608 His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
 609 Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 610 Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 611 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala

612 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 613 Ala Pro Ala Leu Gln Pro (SEQ ID NO:186);
 614
 615
 616 Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
 617 Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
 618 Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
 619 Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
 620 Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg
 621 Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 622 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu
 623 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Tyr Val Glu Gly Gly
 624 Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
 625 Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
 626 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
 627 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
 628 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
 629 Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
 630 Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
 631 Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
 632 His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
 633 Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 634 Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 635 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
 636 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
 637 Ala Pro Ala Leu Gln Pro (SEQ ID NO:187);
 638
 639
 640 Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln
 641 Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln
 642 Ala Gln Glu Gln Gln Gly Gly Gly Ser Asn Cys Ser Ile Met Ile
 643 Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu
 644 Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp
 645 Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val
 646 Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
 647 Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Tyr Val Glu Gly Gly
 648 Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn
 649 Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala
 650 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
 651 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu
 652 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Ser Gly Gly
 653 Ser Gly Gly Ser Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
 654 Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
 655 Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
 656 His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
 657 Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 658 Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser

659 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
660 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met
661 Ala Pro Ala Leu Gln Pro (SEQ ID NO:189);
662
663
664 Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met
665 Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala
666 Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg
667 Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
668 His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu
669 Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
670 Gln Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys
671 Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro
672 Ala Pro Leu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
673 Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
674 Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
675 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
676 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
677 His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
678 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
679 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
680 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
681 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
682 Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
683 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
684 Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
685 Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
686 (SEQ ID NO:190);
687
688
689 Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys
690 Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile
691 Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr
692 Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln Gly Gly Gly Ser
693 Gly Gly Gly Ser Gly Gly Gly Ser Asn Cys Ser Ile Met Ile Asp
694 Glu Ile Ile His His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp
695 Pro Asn Asn Leu Asn Asp Glu Asp Val Ser Ile Leu Met Asp Arg
696 Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala Val Lys
697 Asn Leu Glu Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro
698 Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu
699 Ser His Lys Ser Pro Asn Met Ala Thr Gln Gly Ala Met Pro Ala
700 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
701 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
702 His Leu Ala Gln Pro Ser Gly Gly Ser Gly Gly Ser Gln Ser Phe
703 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
704 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
705 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp

706 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
707 Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
708 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
709 Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
710 Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro;
711 (SEQ ID NO:191)
712
713
714 MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
715 ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn
716 LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
717 AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
718 ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
719 PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
720 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
721 SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
722 GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
723 TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
724 LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
725 LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer
726 LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
727 CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
728 GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
729 AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro;
730 (SEQ ID NO:199)
731
732 MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
733 ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn
734 LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
735 AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
736 ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
737 PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
738 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
739 SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
740 GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
741 TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
742 GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
743 LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
744 GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
745 LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
746 AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
747 AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
748 GlnPro (SEQ ID NO:200);
749
750
751 MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
752 ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetGluAsnAsn

753 LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
754 AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
755 ThrArgHisProIleIleIleArgAspGlyAspTrpAsnGluPheArgArgLysLeuThr
756 PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
757 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
758 SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
759 GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
760 TyrArgValLeuArgHisLeuAlaGlnProSerGlyGlySerGlyGlySerGlnSerPhe
761 LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGlu
762 LysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuGlyHisSer
763 LeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly
764 CysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGlu
765 GlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe
766 AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnPro;
767 (SEQ ID NO:201)

768
769
770 MetAlaAsnCysSerAsnMetIleAspGluIleIleThrHisLeuLysGlnProProLeu
771 ProLeuLeuAspPheAsnAsnLeuAsnGlyGluAspGlnAspIleLeuMetAspAsnAsn
772 LeuArgArgProAsnLeuGluAlaPheAsnArgAlaValLysSerLeuGlnAsnAlaSer
773 AlaIleGluSerIleLeuLysAsnLeuLeuProCysLeuProLeuAlaThrAlaAlaPro
774 ThrArgHisProIleHisIleLysAspGlyAspTrpAsnGluPheArgArgLysLeuThr
775 PheTyrLeuLysThrLeuGluAsnAlaGlnAlaGlnGlnTyrValGluGlyGlyGlyGly
776 SerProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGlu
777 SerHisLysSerProAsnMetAlaThrGlnGlyAlaMetProAlaPheAlaSerAlaPhe
778 GlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValSer
779 TyrArgValLeuArgHisLeuAlaGlnProThrProLeuGlyProAlaSerSerLeuPro
780 GlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla
781 LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeu
782 GlyHisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGln
783 LeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGln
784 AlaLeuGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAspVal
785 AlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeu
786 GlnPro (SEQ ID NO:202);

787
788
789 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
790 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
791 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
792 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
793 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
794 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
795 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
796 HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
797 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
798 GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
799 ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe

800 GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
801 ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
802 ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
803 GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
804 AlaArgGlyGlnLeu (SEQ ID NO:221);
805
806

807 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
808 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
809 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
810 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
811 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
812 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
813 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
814 HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
815 AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
816 MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyAsnMetAlaSerProAla
817 ProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHis
818 SerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeuProAla
819 ValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIle
820 LeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyPro
821 ThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAla
822 LeuGlnSerLeuLeu (SEQ ID NO:222);
823
824

825 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
826 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
827 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
828 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
829 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
830 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
831 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
832 HisLysSerProAsnMetGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGly
833 GlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGln
834 GlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu
835 ArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPhe
836 GlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeu
837 SerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluVal
838 HisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLys
839 ThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlu
840 GlyValMetAlaAlaArgGlyGlnLeu (SEQ ID NO:223);
841
842

843 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
844 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
845 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
846 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer

847 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
848 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
849 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
850 HisLysSerProAsnMetGlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLys
851 AspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPheLeu
852 MetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMet
853 AlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuArgAspSer
854 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
855 LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
856 AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
857 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
858 LeuLeuGlyAlaLeuGlnSerLeuLeu (SEQ ID NO:234);

859
860
861 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
862 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
863 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
864 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
865 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
866 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
867 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
868 HisLysSerProAsnMetGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu
869 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr
870 LeuCysValArgGluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAla
871 CysAspLeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeu
872 SerGlnCysProGluValHisProLeuProThrProValLeuLeuProAlaValAspPhe
873 SerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAla
874 ValThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeu
875 SerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSer
876 LeuLeuGlyThrGlnLeuProProGln (SEQ ID NO:235);

877
878
879 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
880 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
881 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
882 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
883 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
884 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
885 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
886 HisLysSerProAsnMetAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
887 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArg
888 GluPheGlyGlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArg
889 ValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysPro
890 GluValHisProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu
891 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeu
892 LeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeu
893 GlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThr

894 GlnLeuProProGlnGlyArgThrThr (SEQ ID NO:236);
895
896
897 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
898 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
899 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
900 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
901 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
902 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
903 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
904 HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg
905 GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
906 GlyAsnGlyGlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSer
907 LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
908 ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
909 GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
910 ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu
911 SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
912 ProGlnGlyArgThrThrAlaHisLys (SEQ ID NO:237);
913
914
915 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
916 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
917 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
918 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
919 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
920 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
921 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
922 HisLysSerProAsnMetAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
923 ArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGlyGlyAsnGly
924 GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
925 ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
926 ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
927 GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
928 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
929 ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGly
930 ArgThrThrAlaHisLysAspProAsn (SEQ ID NO:238);
931
932
933 AlaAsnCysSerIleMetIleAspGluIleIleHisHisLeuLysArgProProAlaPro
934 LeuLeuAspProAsnAsnLeuAsnAspGluAspValSerIleLeuMetAspArgAsnLeu
935 ArgLeuProAsnLeuGluSerPheValArgAlaValLysAsnLeuGluAsnAlaSerGly
936 IleGluAlaIleLeuArgAsnLeuGlnProCysLeuProSerAlaThrAlaAlaProSer
937 ArgHisProIleIleIleLysAlaGlyAspTrpGlnGluPheArgGluLysLeuThrPhe
938 TyrLeuValThrLeuGluGlnAlaGlnGluGlnGlnTyrValGluGlyGlyGlyGlySer
939 ProGlyGluProSerGlyProIleSerThrIleAsnProSerProProSerLysGluSer
940 HisLysSerProAsnMetAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArg

941 GlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuCysValArgGluPheGly
 942 GlyAsnMetAlaSerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeu
 943 ArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuPro
 944 ThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGlu
 945 GluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAla
 946 AlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGln
 947 ValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnGlyArgThrThrAla
 948 HisLys (SEQ ID NO:239);
 949
 950
 951 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 952 Leu
 953 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 954 Asp
 955 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 956 Asn
 957 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 958 Ser
 959 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 960 Ser
 961 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 962 Gly
 963 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 964 Thr
 965 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 966 Gly
 967 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 968 Ser
 969 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
 970 Gly
 971 151 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
 972 Glu
 973 166 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 974 Lys
 975 181 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 976 Leu
 977 196 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 978 Cys
 979 211 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
 980 His
 981 226 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
 982 Gly
 983 241 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
 984 Asp
 985 256 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 986 Leu

987 271 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
 988 Ala
 989 286 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
 990 Ala
 991 301 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
 992 Arg
 993 316 His Leu Ala Gln Pro Asp Met Ala Thr Pro (SEQ ID NO:271);
 994
 995
 996 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 997 Leu
 998 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 999 Asp
 1000 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1001 Asn
 1002 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1003 Ser
 1004 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1005 Ser
 1006 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1007 Gly
 1008 31 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1009 Thr
 1010 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1011 Gly
 1012 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1013 Ser
 1014 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
 1015 Gly
 1016 151 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
 1017 Glu
 1018 176 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 1019 Lys
 1020 191 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 1021 Leu
 1022 206 Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 1023 Cys
 1024 221 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu
 1025 His
 1026 236 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu
 1027 Gly
 1028 251 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
 1029 Asp
 1030 266 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu
 1031 Leu
 1032 281 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
 1033 Ala

1034 296 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
 1035 Ala
 1036 311 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
 1037 Arg
 1038 326 His Leu Ala Gln Pro Asp Met Ala Thr Pro (SEQ ID NO:272);
 1039
 1040
 1041 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1042 Leu
 1043 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1044 Asp
 1045 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1046 Asn
 1047 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1048 Ser
 1049 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1050 Ser
 1051 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1052 Gly
 1053 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1054 Thr
 1055 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1056 Gly
 1057 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1058 Ser
 1059 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Phe
 1060 Leu
 1061 151 Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
 1062 Ala
 1063 166 Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His
 1064 Pro
 1065 181 Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp
 1066 Ala
 1067 196 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly
 1068 Cys
 1069 211 Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu
 1070 Leu
 1071 226 Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
 1072 Asp
 1073 241 Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp
 1074 Gln
 1075 256 Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr
 1076 Gln
 1077 271 Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala
 1078 Gly
 1079 286 Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val
 1080 Ser

1081 301 Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr
 1082 Pro
 1083 316 Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser (SEQ ID NO:273);
 1084
 1085
 1086 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1087 Leu
 1088 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1089 Asp
 1090 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1091 Asn
 1092 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1093 Ser
 1094 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1095 Ser
 1096 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1097 Gly
 1098 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1099 Thr
 1100 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1101 Gly
 1102 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1103 Ser
 1104 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Glu
 1105 Gln
 1106 151 Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys
 1107 Leu
 1108 166 Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu
 1109 Leu
 1110 181 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
 1111 Pro
 1112 196 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 1113 Ser
 1114 211 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
 1115 Ile
 1116 226 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
 1117 Val
 1118 241 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
 1119 Gly
 1120 256 Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
 1121 Phe
 1122 271 Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
 1123 Ser
 1124 286 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
 1125 His
 1126 301 Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser
 1127 Ser

1128 316 Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu (SEQ ID NO:274);
1129
1130
1131 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
1132 Leu
1133 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
1134 Asp
1135 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
1136 Asn
1137 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
1138 Ser
1139 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
1140 Ser
1141 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
1142 Gly
1143 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
1144 Thr
1145 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
1146 Gly
1147 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
1148 Ser
1149 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
1150 Leu
1151 151 Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
1152 Pro
1153 166 Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
1154 Ser
1155 181 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly
1156 Ile
1157 196 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp
1158 Val
1159 211 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
1160 Gly
1161 226 Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala
1162 Phe
1163 241 Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala
1164 Ser
1165 256 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg
1166 His
1167 271 Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser
1168 Ser
1169 286 Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg
1170 Lys
1171 301 Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala
1172 Thr
1173 316 Tyr Lys Leu Cys His Pro Glu Glu Leu Val (SEQ ID NO:275);
1174

1175
 1176 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1177 Leu
 1178 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1179 Asp
 1180 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1181 Asn
 1182 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1183 Ser
 1184 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1185 Ser
 1186 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1187 Gly
 1188 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1189 Thr
 1190 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1191 Gly
 1192 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1193 Ser
 1194 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Pro
 1195 Leu
 1196 151 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu
 1197 Ser
 1198 166 Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln
 1199 Ala
 1200 181 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr
 1201 Leu
 1202 196 Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln
 1203 Met
 1204 211 Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly
 1205 Ala
 1206 226 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly
 1207 Val
 1208 241 Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr
 1209 Arg
 1210 256 Val Leu Arg His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu
 1211 Gly
 1212 271 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu
 1213 Glu
 1214 286 Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu
 1215 Lys
 1216 301 Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
 1217 Leu
 1218 316 Leu Gly His Ser Leu Gly Ile Pro Trp Ala (SEQ ID NO:276);
 1219
 1220

1221 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1222 Leu
 1223 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1224 Asp
 1225 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1226 Asn
 1227 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1228 Ser
 1229 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1230 Ser
 1231 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1232 Gly
 1233 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1234 Thr
 1235 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1236 Gly
 1237 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1238 Ser
 1239 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Gln
 1240 Ala
 1241 151 Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu
 1242 Phe
 1243 166 Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro
 1244 Glu
 1245 181 Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
 1246 Phe
 1247 196 Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
 1248 Pro
 1249 211 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser
 1250 Ala
 1251 226 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu
 1252 Gln
 1253 241 Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala
 1254 Gln
 1255 256 Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro
 1256 Gln
 1257 271 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln
 1258 Gly
 1259 286 Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys
 1260 Leu
 1261 301 Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
 1262 Ile
 1263 316 Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser (SEQ ID NO:277);
 1264
 1265
 1266 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1267 Leu

1268 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1269 Asp
 1270 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1271 Asn
 1272 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1273 Ser
 1274 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1275 Ser
 1276 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1277 Gly
 1278 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1279 Thr
 1280 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1281 Gly
 1282 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1283 Ser
 1284 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
 1285 Gln
 1286 151 Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu
 1287 Tyr
 1288 166 Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu
 1289 Gly
 1290 181 Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala
 1291 Thr
 1292 196 Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala
 1293 Leu
 1294 211 Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
 1295 Gln
 1296 226 Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
 1297 Phe
 1298 241 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 1299 Asp
 1300 256 Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
 1301 Phe
 1302 271 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 1303 Gly
 1304 286 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys
 1305 His
 1306 301 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
 1307 Trp
 1308 316 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala (SEQ ID NO:278);
 1309
 1310
 1311 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1312 Leu
 1313 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1314 Asp

1315 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1316 Asn
 1317 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1318 Ser
 1319 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1320 Ser
 1321 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1322 Gly
 1323 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1324 Thr
 1325 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1326 Gly
 1327 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1328 Ser
 1329 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Leu
 1330 Ala
 1331 151 Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln
 1332 Gly
 1333 166 Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro
 1334 Thr
 1335 181 Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr
 1336 Ile
 1337 196 Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln
 1338 Pro
 1339 211 Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg
 1340 Arg
 1341 226 Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu
 1342 Glu
 1343 241 Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Asp Met
 1344 Ala
 1345 256 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
 1346 Leu
 1347 271 Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala
 1348 Ala
 1349 286 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
 1350 Glu
 1351 301 Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala
 1352 Pro
 1353 316 Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln (SEQ ID NO:279);
 1354
 1355
 1356 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1357 Leu
 1358 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1359 Asp
 1360 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1361 Asn

1362 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1363 Ser
 1364 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1365 Ser
 1366 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1367 Gly
 1368 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1369 Thr
 1370 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1371 Gly
 1372 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1373 Ser
 1374 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Glu
 1375 Leu
 1376 151 Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro
 1377 Ala
 1378 166 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val
 1379 Ala
 1380 181 Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu
 1381 Arg
 1382 196 His Leu Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala
 1383 Ser
 1384 211 Ser Leu Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val
 1385 Arg
 1386 226 Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys
 1387 Ala
 1388 241 Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly
 1389 His
 1390 256 Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser
 1391 Gln
 1392 271 Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly
 1393 Leu
 1394 286 Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
 1395 Pro
 1396 301 Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
 1397 Asp
 1398 316 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu (SEQ ID NO:280);
 1399
 1400
 1401 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1402 Leu
 1403 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1404 Asp
 1405 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1406 Asn
 1407 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1408 Ser

1409 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1410 Ser
 1411 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1412 Gly
 1413 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1414 Thr
 1415 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1416 Gly
 1417 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1418 Ser
 1419 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Gly
 1420 Met
 1421 151 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
 1422 Ala
 1423 166 Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
 1424 His
 1425 181 Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
 1426 Leu
 1427 196 Ala Gln Pro Asp Met Ala Thr Pro Leu Gly Pro Ala Ser Ser
 1428 Leu
 1429 211 Pro Gln Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys
 1430 Ile
 1431 226 Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
 1432 Tyr
 1433 241 Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser
 1434 Leu
 1435 256 Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala
 1436 Leu
 1437 271 Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe
 1438 Leu
 1439 286 Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu
 1440 Leu
 1441 301 Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
 1442 Ala
 1443 316 Thr Thr Ile Trp Gln Gln Met Glu Glu Leu (SEQ ID NO:281);
 1444 and
 1445
 1446
 1447 1 Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
 1448 Leu
 1449 16 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn
 1450 Asp
 1451 31 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro
 1452 Asn
 1453 46 Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala
 1454 Ser

1455 61 Gly Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro
 1456 Ser
 1457 76 Ala Thr Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala
 1458 Gly
 1459 91 Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val
 1460 Thr
 1461 106 Leu Glu Gln Ala Gln Glu Gln Gln Tyr Val Glu Gly Gly Gly
 1462 Gly
 1463 121 Ser Pro Gly Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro
 1464 Ser
 1465 136 Pro Pro Ser Lys Glu Ser His Lys Ser Pro Asn Met Ala Ser
 1466 Phe
 1467 151 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
 1468 Asp
 1469 166 Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
 1470 Phe
 1471 181 Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp
 1472 Gly
 1473 196 Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys
 1474 His
 1475 211 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
 1476 Trp
 1477 226 Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala
 1478 Gly
 1479 241 Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
 1480 Leu
 1481 256 Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr
 1482 Leu
 1483 271 Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile
 1484 Trp
 1485 286 Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
 1486 Thr
 1487 301 Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg
 1488 Ala
 1489 316 Gly Gly Val Leu Val Ala Ser His Leu Gln (SEQ ID NO:282).

1 16. The hematopoietic protein as recited in claim 1
 2 wherein said c-mpl receptor agonist is selected from the group
 3 consisting of:

4
 5 MetAlaGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHis
 6 LeuLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeuAlaValArg
 7 GluPheGlyGlyAsnMetAlaSerProAlaProProAlaAlaAspLeuArgValLeuSer
 8 LysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis
 9 ProLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThr
 10 GlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGly
 11 ValMetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeu

12 SerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuPro
13 ProGln (SEQ ID NO:284); and
14
15 MetAlaGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu
16 LeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrThr
17 AlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysVal
18 ArgPheLeuMetLeuValGlyGlySerThrLeuAlaValArgGluPheGlyGlyAsnMet
19 AlaSerProAlaProProAlaAlaAspLeuArgValLeuSerLysLeuLeuArgAspSer
20 HisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProVal
21 LeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLys
22 AlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly
23 GlnLeu (SEQ ID NO:285)

1 17. The hematopoietic protein of claim 1, 2, 3, 4, 5, 6,
2 7, 8, 9, 10, 11 or 12 wherein said colony stimulating factor
3 is selected from the group consisting of GM-CSF, G-CSF, G-CSF
4 Ser¹⁷, c-mpl ligand (TPO), M-CSF, erythropoietin (EPO), IL-1,
5 IL-4, IL-2, IL-3, IL-5, IL 6, IL-7, IL-8, IL-9, IL-10, IL-11,
6 IL-12, IL-13, IL-15, LIF, flt3/flk2 ligand, human growth
7 hormone, B-cell growth factor, B-cell differentiation factor,
8 eosinophil differentiation factor and stem cell factor (SCF).

1 18. The hematopoietic protein of claim 17 wherein said
2 colony stimulating factor is selected from the group
3 consisting of G-CSF, G-CSF Ser¹⁷ and c-mpl ligand (TPO).

1 19. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 1.

1 20. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 2.

1 21. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 3.

1 22. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 4.

1 23. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 5.

1 24. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 6.

1 25. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 7.

1 26. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 8.

1 27. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 9.

1 28. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 10.

1 29. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 11.

1 30. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 12.

1 31. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 13.

1 32. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 14.

1 33. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 15.

1 34. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 16.

1 35. A nucleic acid molecule encoding said hematopoietic
2 protein of claim 17.

1 36. The nucleic acid molecule according to claim 30
2 selected from group consisting of:
3
4

5 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
6 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
7 101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
8 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
9 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
10 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
11 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
12 351 CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTT
13 401 ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC
14 451 ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCC TGCAGCTGGC
15 501 AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC CAGGGGCTCC
16 551 TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA
17 601 CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA
18 651 AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG
19 701 CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTGCTAGC
20 751 CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC
21 801 GCAGCCCTCT GGCGGCTCTG GCGGCTCTCA GAGCTTCCTG CTCAAGTCTT
22 851 TAGAGCAAGT GAGAAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
23 901 CTGTGTGCCA CCTAATAA (SEQ ID NO:94);
24
25

26 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
27 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
28 101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
29 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
30 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
31 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
32 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
33 351 CGGTGGAGGC TCCCCGGGTG AACCCTCTGG TCCAATCTCT ACTATCAACC
34 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTACAAG
35 451 CTGTGCCACC CCGAGGAGCT GGTGCTGCTC GGAACTCTC TGGGCATCCC
36 501 CTGGGCTCCC CTGAGCTCCT GCCCAGCCA GGCCCTGCAG CTGGCAGGCT
37 551 GCTTGAGCCA ACTCCATAGC GGCTTTTCC TCTACCAGGG GCTCCTGCAG
38 601 GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA
39 651 GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC
40 701 TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT GCCGGCCTTC
41 751 GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG CTAGCCATCT
42 801 GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC
43 851 CCTCTGGCGG CTCTGGCGGC TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG

44 901 CAAGTGAGAA AGATCCAGGG CGATGGCGCA GCGCTCCAGG AGAAGCTGTG
45 951 TGCCACCTAA TAA (SEQ ID NO:95);
46
47
48 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
49 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
50 101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
51 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
52 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
53 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
54 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
55 351 CGGTGGAGGC TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC
56 401 CCGAGTTGGG TCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
57 451 GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
58 501 GCAGCCCACC CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC
59 551 GGGCAGGAGG GGTCTTGTT GCTAGCCATC TGCAGAGCTT CCTGGAGGTG
60 601 TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCTCTGGCG GCTCTGGCGG
61 651 CTCTCAGAGC TTCTGCTCA AGTCTTTAGA GCAAGTGAGA AAGATCCAGG
62 701 GCGATGGCGC AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC
63 751 CACCCCGAGG AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC
64 801 TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA
65 851 GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG
66 901 GAAGGGATAT CCTAATAA (SEQ ID NO:96);
67
68
69 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
70 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
71 101 CTATCCTGAT GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
72 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
73 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
74 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
75 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
76 351 CGGTGGAGGC TCCCCGGGTG AACCCTCTGG TCCAATCTCT ACTATCAACC
77 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCGAG
78 451 TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
79 501 CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC
80 551 CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
81 601 GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
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394 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 395 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 396 101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 397 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 398 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 399 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 400 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 401 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 402 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTCCCGAG
 403 451 TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC
 404 501 CACCATCTGG CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC
 405 551 CCACCCAGGG TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA
 406 601 GGAGGGGTCC TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA
 407 651 CCGCGTTCTA CGCCACCTTG CGCAGCCCGG CGGCGGCTCT GACATGGCTA
 408 701 CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT
 409 751 TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC TCCAGGAGAA
 410 801 GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG GTGCTGCTCG
 411 851 GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG
 412 901 GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCTT
 413 951 CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCTAA TAA
 414 (SEQ ID NO:156);
 415
 416

417 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 418 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 419 101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA

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420 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
421 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
422 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
423 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
424 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
425 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTTCTGCT
426 451 TTCCAGCGCC GGGCAGGAGG GGTCCTGGTT GCTAGCCATC TGCAGAGCTT
427 501 CCTGGAGGTG TCGTACCGCG TTCTACGCCA CCTTGCGCAG CCCGGCGGCG
428 551 GCTCTGACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCAGAGC
429 601 TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC
430 651 AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG
431 701 AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC
432 751 TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA
433 801 TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT
434 851 CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC
435 901 TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC
436 951 CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCCTAA TAA

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(SEQ ID NO:157);

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440 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
441 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
442 101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
443 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
444 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
445 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
446 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
447 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
448 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTATGGCC
449 451 CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT
450 501 CCAGCGCCGG GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC
451 551 TGGAGGTGTC GTACCGCGTT CTACGCCACC TTGCGCAGCC CGGCGGCGGC
452 601 TCTGACATGG CTACACCATT AGGCCCTGCC AGCTCCCTGC CCCAGAGCTT
453 651 CCTGCTCAAG TCTTTAGAGC AAGTGAGGAA GATCCAGGGC GATGGCGCAG
454 701 CGTCCAGGA GAAGCTGTGT GCCACCTACA AGCTGTGCCA CCCCAGAGGAG
455 751 CTGGTGCTGC TCGGACACTC TCTGGGCATC CCCTGGGCTC CCCTGAGCTC
456 801 CTGCCCCAGC CAGGCCCTGC AGCTGGCAGG CTGCTTGAGC CAACTCCATA
457 851 GCGGCCTTTT CCTCTACCAG GGGCTCCTGC AGGCCCTGGA AGGGATATCC
458 901 CCCGAGTTGG GTCCCACCTT GGACACACTG CAGCTGGACG TCGCCGACTT
459 951 TGCCACCACC ATCTGGCAGC AGATGGAAGA ACTGGGATAA TAA

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(SEQ ID NO:158);

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463 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
464 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
465 101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
466 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG

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467 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
468 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
469 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
470 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
471 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GTCTACCCAG
472 451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
473 501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCG TACCGCGTTC
474 551 TACGCCACCT TGCGCAGCCC GGCGGCGGCT CTGACATGGC TACACCATTA
475 601 GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA
476 651 AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG
477 701 CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT CGGACACTCT
478 751 CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC AGGCCCTGCA
479 801 GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC CTCTACCAGG
480 851 GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG TCCCACCTTG
481 901 GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA TCTGGCAGCA
482 951 GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCTAA TAA

(SEQ ID NO:159);

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486 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCT
487 TTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT
488 CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGT
489 ATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCT
490 CGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
491 TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCC
492 CCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCT
493 CATAAATCTCCAAACATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGA
494 CAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG
495 GGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTC
496 CGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTC
497 GGCGGCAACATGGCGTCTCCGGCGCCGCTGCTTGTGACCTCCGAGTCCTCAGTAAACTG
498 CTTCTGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCCAGAGGTTACCCCTTTG
499 CCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATG
500 GAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATG
501 GCAGCACGGGGACAACCTG (SEQ ID NO:124);

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503

504 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCT
505 TTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT
506 CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGT
507 ATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCT
508 CGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTC
509 TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCC
510 CCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCT
511 CATAAATCTCCAAACATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAG
512 GATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTG
513 ATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCG

514 GCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTT
515 CACAGCAGACTGAGCCAGTGCCCAGAGGTTACCCCTTTGCCTACACCTGTCTGCTGCCT
516 GCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGAC
517 ATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGA
518 CCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGG
519 GCCCTGCAGAGCCTCCTT (SEQ ID NO:125);

520
521
522 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCT
523 TTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT
524 CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGT
525 ATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCT
526 CGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTT
527 TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCC
528 CCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCT
529 CATAAATCTCCAAACATGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTG
530 AGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTTAGGAGGGTCCACC
531 CTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCGGCGCCGCTGCTTGTGACCTC
532 CGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGC
533 CCAGAGGTTACCCCTTTGCCTACACCTGTCTGCTGCCTGCTGTGGACTTTAGCTTGGGA
534 GAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTT
535 CTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTC
536 CTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGGA
537 ACCCAGCTTCCTCCACAG (SEQ ID NO:126);

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539
540 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCT
541 TTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT
542 CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGT
543 ATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCT
544 CGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTT
545 TATCTGGTTACCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCC
546 CCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCT
547 CATAAATCTCCAAACATGGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACAC
548 CTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTTAGGAGGGTCCACCCTCTGCGTCAGG
549 GAATTCGGCGGCAACATGGCGTCTCCGGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGT
550 AAAGTGGTTCGTGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTTAC
551 CCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACC
552 CAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGA
553 GTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTT
554 TCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAAACCAGCTTCCT
555 CCACAGGGCAGGACCACA (SEQ ID NO:127);

556
557
558 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCT
559 TTGCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTT
560 CGACTTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGT

561 ATTGAGGCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCT
562 CGACATCCAATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTC
563 TATCTGGTTACCCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCC
564 CCGGGTGAACCGTCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCT
565 CATAAATCTCCAAACATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGA
566 GGAAAGGTGCGTTTCCTGATGCTTG TAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGC
567 GGCAACATGGCGTCTCCGGCGCCGCTGCTTG TAGCCTCCGAGTCCTCAGTAAACTGCTT
568 CGTGACTCCCATGTCCCTTACAGCAGACTGAGCCAGTGCCAGAGGTTCCACCCTTTGCCT
569 ACACCTGTCTGCTGCCTGCTGTGGACTTTAGCTTG GGGAGAATGGAAAACCCAGATGGAG
570 GAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCA
571 GCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAG
572 GTCCGTCTCCTCCTTG GGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCTCCACAGGGC
573 AGGACCACAGCTCACAAG (SEQ ID NO:128);
574

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576 1 ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
577 51 GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
578 101 ATATCCTAAT GGACAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
579 151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
580 201 AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
581 251 CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
582 301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
583 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
584 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
585 451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
586 501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG TACCGCGTTC
587 551 TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
588 601 CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
589 651 GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
590 701 TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
591 751 TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
592 801 CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
593 851 CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
594 901 GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
595 951 GCAGCCCTAA TAA (SEQ ID NO:114);

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597
598 1 ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
599 51 GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
600 101 ATATCCTGAT GGAAAATAAC CTTCGTCGTC CAAACCTCGA GGCATTCAAC
601 151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
602 201 AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC ACGCGACATC
603 251 CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
604 301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
605 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
606 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
607 451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT

608 501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG TACCGCGTTC
 609 551 TACGCCACCT TGCGCAGCCC ACACCATTTGG GCCCTGCCAG CTCCCTGCCC
 610 601 CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
 611 651 TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
 612 701 CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
 613 751 CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
 614 801 ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
 615 851 GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
 616 901 GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
 617 951 CCCTGCCCTG CAGCCCTAAT AA (SEQ ID NO:115);

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620 1 ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
 621 51 GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
 622 101 ATATCCTGAT GGAAAATAAC CTTTCGTCGTC CAAACCTCGA GGCATTCAAC
 623 151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
 624 201 AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC ACGCGACATC
 625 251 CAATCATCAT CCGTGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
 626 301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
 627 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 628 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
 629 451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
 630 501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG TACCGCGTTC
 631 551 TACGCCACCT TGCGCAGCCC TCTGGCGGCT CTGGCGGCTC TCAGAGCTTC
 632 601 CTGCTCAAGT CTTTAGAGCA AGTGAGAAAG ATCCAGGGCG ATGGCGCAGC
 633 651 GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC
 634 701 TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC
 635 751 TGCCCCAGCC AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG
 636 801 CGGCCTTTTC CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC
 637 851 CCGAGTTGGG TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT
 638 901 GCCACCACCA TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT
 639 951 GCAGCCCTAA TAA (SEQ ID NO:116);

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642 1 ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA
 643 51 GCCACCGCTG CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG
 644 101 ATATCCTAAT GGACAATAAC CTTTCGTCGTC CAAACCTCGA GGCATTCAAC
 645 151 CGTGCTGTCA AGTCTCTGCA GAATGCATCA GCAATTGAGA GCATTCTTAA
 646 201 AAATCTCCTG CCATGTCTGC CGCTAGCCAC GGCCGCACCC ACGCGACATC
 647 251 CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC
 648 301 TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT ACGTAGAGGG
 649 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 650 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTACCCAG
 651 451 GGTGCCATGC CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT
 652 501 CCTGGTTGCT AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG TACCGCGTTC
 653 551 TACGCCACCT TGCGCAGCCC ACACCATTTGG GCCCTGCCAG CTCCCTGCCC

654 601 CAGAGCTTCC TGCTCAAGTC TTTAGAGCAA GTGAGAAAGA TCCAGGGCGA
 655 651 TGGCGCAGCG CTCCAGGAGA AGCTGTGTGC CACCTACAAG CTGTGCCACC
 656 701 CCGAGGAGCT GGTGCTGCTC GGACACTCTC TGGGCATCCC CTGGGCTCCC
 657 751 CTGAGCTCCT GCCCCAGCCA GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA
 658 801 ACTCCATAGC GGCCTTTTCC TCTACCAGGG GCTCCTGCAG GCCCTGGAAG
 659 851 GGATATCCCC CGAGTTGGGT CCCACCTTGG ACACACTGCA GCTGGACGTC
 660 901 GCCGACTTTG CCACCACCAT CTGGCAGCAG ATGGAAGAAC TGGGAATGGC
 661 951 CCCTGCCCTG CAGCCCTAAT AA (SEQ ID NO:117);
 662
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 664 1 ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT
 665 51 GGACCGAAAC CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA
 666 101 AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA
 667 151 CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC CAATCATCAT
 668 201 CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG TTCTATCTGG
 669 251 TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TAACTGCTCT
 670 301 ATAATGATCG ATGAAATTAT ACATCACTTA AAGAGACCAC CTGCACCTTT
 671 351 GTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 672 401 CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 673 451 ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 674 501 GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 675 551 CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 676 601 TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 677 651 CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 678 701 ACCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 679 751 CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 680 801 CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 681 851 AAGGGATATC CCCCGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 682 901 GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 683 951 GGCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:86);
 684
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 686 1 ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTGTAATC TCCAACCATG
 687 51 TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG
 688 101 CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC
 689 151 CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTAACT GCTCTATAAT
 690 201 GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA CCTTTGCTGG
 691 251 ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC
 692 301 CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA
 693 351 ATACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GGTCCAATCT
 694 401 CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 695 451 ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 696 501 GGCAGGAGGG GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 697 551 CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 698 601 TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 699 651 CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 700 701 ACCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT

701 751 CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 702 801 CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 703 851 AAGGGATATC CCCCAGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 704 901 GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 705 951 GGCCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:87);
 706
 707
 708 1 ATGGCTGCAC CCTCTCGACA TCCAATCATC ATCAAGGCAG GTGACTGGCA
 709 51 AGAATTCCGG GAAAAACTGA CGTTCTATCT GGTTACCCTT GAGCAAGCGC
 710 101 AGGAACAACA GGGTGGTGGC TCTAACTGCT CTATAATGAT CGATGAAATT
 711 151 ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT
 712 201 CAATGACGAA GACGTCTCTA TCCTGATGGA CCGAAACCTT CGACTTCCAA
 713 251 ACCTGGAGAG CTTCGTAAGG GCTGTCAAGA ACTTAGAAAA TGCATCAGGT
 714 301 ATTGAGGCAA TTCTTCGTAA TCTCCAACCA TGTCTGCCCT CTGCCACGGC
 715 351 CTACGTAGAG GGCGGTGGAG GCTCCCCGGG TGAACCGTCT GTTCCAATCT
 716 401 CTACTATCAA CCCGTCTCCT CCGTCTAAAG AATCTCATAA ATCTCCAAAC
 717 451 ATGGCTACCC AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG
 718 501 GGCAGGAGGG GTCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT
 719 551 CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCTCTGGCGG CTCTGGCGGC
 720 601 TCTCAGAGCT TCCTGCTCAA GTCTTTAGAG CAAGTGAGAA AGATCCAGGG
 721 651 CGATGGCGCA GCGCTCCAGG AGAAGCTGTG TGCCACCTAC AAGCTGTGCC
 722 701 ACCCCGAGGA GCTGGTGCTG CTCGGACACT CTCTGGGCAT CCCCTGGGCT
 723 751 CCCCTGAGCT CCTGCCCCAG CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG
 724 801 CCAACTCCAT AGCGGCCTTT TCCTCTACCA GGGGCTCCTG CAGGCCCTGG
 725 851 AAGGGATATC CCCCAGAGTTG GGTCCCACCT TGGACACACT GCAGCTGGAC
 726 901 GTCGCCGACT TTGCCACCAC CATCTGGCAG CAGATGGAAG AACTGGGAAT
 727 951 GGCCCCCTGCC CTGCAGCCCT AATAA (SEQ ID NO:88);
 728
 729
 730 1 ATGGCTCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT
 731 51 GGACCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA
 732 101 AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG TAATCTCCAA
 733 151 CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC CAATCATCAT
 734 201 CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG TTCTATCTGG
 735 251 TTACCCTTGA GCAAGCGCAG GAACAACAGG GTGGTGGCTC TGGCGGTGGC
 736 301 AGCGGCGGCG GTTCTAACTG CTCTATAATG ATCGATGAAA TTATACATCA
 737 351 CTTAAAGAGA CCACCTGCAC CTTTGTACGT AGAGGGCGGT GGAGGCTCCC
 738 401 CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
 739 451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
 740 501 CTTCGCCTCT GCTTTCAGC GCCGGGCAGG AGGGGTCTCT GTTGCTAGCC
 741 551 ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTCTACG CCACCTTGCG
 742 601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
 743 651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
 744 701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
 745 751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
 746 801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCTCT
 747 851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC

748 901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
749 951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
750 (SEQ ID NO:90);
751
752
753 1 ATGGCTAATG CATCAGGTAT TGAGGCAATT CTTCGTAATC TCCAACCATG
754 51 TCTGCCCTCT GCCACGGCCG CACCCTCTCG ACATCCAATC ATCATCAAGG
755 101 CAGGTGACTG GCAAGAATTC CGGGAAAAAC TGACGTTCTA TCTGGTTACC
756 151 CTTGAGCAAG CGCAGGAACA ACAGGGTGGT GGCTCTGGCG GTGGCAGCGG
757 201 CGGCGGTTCT AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA
758 251 AGAGACCACC TGCACCTTTG CTGGACCCGA ACAACCTCAA TGACGAAGAC
759 301 GTCTCTATCC TGATGGACCG AAACCTTCGA CTTCCAAACC TGGAGAGCTT
760 351 CGTAAGGGCT GTCAAGAACT TAGAATACGT AGAGGGCGGT GGAGGCTCCC
761 401 CGGGTGAACC GTCTGGTCCA ATCTCTACTA TCAACCCGTC TCCTCCGTCT
762 451 AAAGAATCTC ATAAATCTCC AAACATGGCT ACCCAGGGTG CCATGCCGGC
763 501 CTTCGCCTCT GCTTTCAGC GCCGGGCAGG AGGGGTCCTG GTTGCTAGCC
764 551 ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
765 601 CAGCCCTCTG GCGGCTCTGG CGGCTCTCAG AGCTTCCTGC TCAAGTCTTT
766 651 AGAGCAAGTG AGAAAGATCC AGGGCGATGG CGCAGCGCTC CAGGAGAAGC
767 701 TGTGTGCCAC CTACAAGCTG TGCCACCCCG AGGAGCTGGT GCTGCTCGGA
768 751 CACTCTCTGG GCATCCCCTG GGCTCCCCTG AGCTCCTGCC CCAGCCAGGC
769 801 CCTGCAGCTG GCAGGCTGCT TGAGCCAACT CCATAGCGGC CTTTTCTCT
770 851 ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA TATCCCCCGA GTTGGGTCCC
771 901 ACCTTGGACA CACTGCAGCT GGACGTCGCC GACTTTGCCA CCACCATCTG
772 951 GCAGCAGATG GAAGAACTGG GAATGGCCCC TGCCCTGCAG CCCTAATAA
773 (SEQ ID NO:91);
774
775 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
776 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
777 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
778 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
779 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
780 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
781 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
782 CATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCC
783 TTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCTCCACAGGGCAGGACCACAGCTCAC
784 AAGGATCCCAATGCCATCTTCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCT
785 GATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCAACATGGCGTCTCCCGCTC
786 CGCCTGCTTGTGACCTCCGAGTCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGC
787 AGACTGAGCCAGTGCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGA
788 CTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAG
789 CAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTG (SEQ ID
790 NO:136);
791
792
793 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
794 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC

795 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
796 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
797 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
798 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
799 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
800 CATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCT
801 TCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
802 ACCCTCTGCGTCAGGGAATTTCGGCAACATGGCGTCTCCCGCTCCGCCTGCTTGTGACCTCCG
803 AGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAG
804 AGGTTACCCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGG
805 AAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGA
806 GGGAGTGATGGCAGCACGGGGACAACCTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGC
807 TTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTT (SEQ ID
808 NO:137);
809
810
811 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
812 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
813 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
814 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
815 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
816 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
817 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
818 CATGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCC
819 TTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCAC
820 AAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCT
821 GATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTTCGGCGGCAACGGCGGCAACATGG
822 CGTCCCCAGCGCCGCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCAT
823 GTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGCT
824 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGG
825 ACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTG
826 (SEQ ID NO:148);
827
828
829 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
830 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
831 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
832 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
833 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
834 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
835 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
836 CATGGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCT
837 TCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCC
838 ACCCTCTGCGTCAGGGAATTTCGGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCTGC
839 TTGTGACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGA
840 GCCAGTGCCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGCTGCCTGCTGTGGACTTTAGC
841 TTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGAC

842 CCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTGGGACCCACTTGCCTCTCATCCC
843 TCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTT
844 (SEQ ID NO:149);

845
846
847 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
848 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
849 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
850 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
851 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
852 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
853 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
854 CATGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGC
855 TCCGAGGAAAGGTGCGTTTCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTC
856 GGCGGCAACGGCGGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAG
857 TAAACTGCTTCGTGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCCAGAGGTTACCC
858 CTTTGCCTACACCTGTCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAG
859 ATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGAT
860 GGCAGCACGGGGACAACCTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGAC
861 AGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAG
862 (SEQ ID NO:150);

863
864
865 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
866 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
867 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
868 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
869 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
870 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
871 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
872 CATGGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGG
873 TCGTTTTCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGC
874 GGCAACATGGCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCTCAGTAACTGCTTCG
875 TGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTACCCCTTTGCCTACAC
876 CTGTCCTGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACC
877 AAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGG
878 ACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCC
879 TCCTTGGGGCCCTGCAGAGCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACA
880 (SEQ ID NO:151);

881
882
883 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
884 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
885 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
886 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
887 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAAACTGACGTTCTATCTGGTTA
888 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG

889 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
890 CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
891 TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACGGCGGCAACATG
892 GCGTCCCCAGCGCCGCCTGCTTGTGACCTCCGAGTCCCTCAGTAAACTGCTTCGTGACTCCCA
893 TGTCTTCACAGCAGACTGAGCCAGTGCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGC
894 TGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAG
895 GACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTGGG
896 ACCCACTTGCTCTCATCCCTCCTGGGGCAGCTTCTTGACAGGTCCGTCTCCTCCTTGGGG
897 CCCTGCAGAGCCTCCTTGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAG

(SEQ ID NO:152);

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901 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
902 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
903 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
904 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
905 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
906 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
907 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
908 CATGGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTG
909 TAGGAGGGTCCACCCTCTGCGTCAGGGAATTTCGGCGGCAACGGCGGCAACATGGCGTCCCCA
910 GCGCCGCTGCTTGTGACCTCCGAGTCCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCA
911 CAGCAGACTGAGCCAGTGCCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGCTGCCTGCTG
912 TGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTG
913 GGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTGGGACCCACTTG
914 CCTCTCATCCCTCCTGGGGCAGCTTCTTGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGA
915 GCCTCCTTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAAT

(SEQ ID NO:153);

916
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918
919 GCTAACTGCTCTATAATGATCGATGAAATTATACATCACTTAAAGAGACCACCTGCACCTTT
920 GCTGGACCCGAACAACCTCAATGACGAAGACGTCTCTATCCTGATGGACCGAAACCTTCGAC
921 TTCCAAACCTGGAGAGCTTCGTAAGGGCTGTCAAGAACTTAGAAAATGCATCAGGTATTGAG
922 GCAATTCTTCGTAATCTCCAACCATGTCTGCCCTCTGCCACGGCCGCACCCTCTCGACATCC
923 AATCATCATCAAGGCAGGTGACTGGCAAGAATTCCGGGAAAACTGACGTTCTATCTGGTTA
924 CCCTTGAGCAAGCGCAGGAACAACAGTACGTAGAGGGCGGTGGAGGCTCCCCGGGTGAACCG
925 TCTGGTCCAATCTCTACTATCAACCCGTCTCCTCCGTCTAAAGAATCTCATAAATCTCCAAA
926 CATGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCC
927 TGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGGAATTCGGCGGCAACATGGCGTCTCCC
928 GCTCCGCCTGCTTGTGACCTCCGAGTCCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCA
929 CAGCAGACTGAGCCAGTGCCCAGAGGTTACCCCTTTGCCTACACCTGTCCTGCTGCCTGCTG
930 TGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTG
931 GGAGCAGTGACCCTTCTGCTGGAGGGAGTGATGGCAGCACGGGGACAACCTGGGACCCACTTG
932 CCTCTCATCCCTCCTGGGGCAGCTTCTTGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGA
933 GCCTCCTTGGAACCCAGGGCAGGACCACAGCTCACAAG

(SEQ ID NO:154);

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936
937 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
938 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
939 101 CTATCCTGAT GGATCGAAAC CTTGCGACTTC CAAACCTGGA GAGCTTCGTA
940 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
941 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
942 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
943 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
944 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
945 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTTTAGGC
946 451 CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT TAGAGCAAGT
947 501 GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG CTGTGTGCCA
948 551 CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG AACTCTCTG
949 601 GGCATCCCCT GGGCTCCCCT GAGCTCCTGC CCCAGCCAGG CCCTGCAGCT
950 651 GGCAGGCTGC TTGAGCCAAC TCCATAGCGG CCTTTTCCTC TACCAGGGGC
951 701 TCCTGCAGGC CCTGGAAGGG ATATCCCCCG AGTTGGGTCC CACCTTGGAC
952 751 AACTGCAGC TGGACGTCGC CGACTTTGCC ACCACCATCT GGCAGCAGAT
953 801 GGAAGAACTG GGAATGGCCC CTGCCCTGCA GCCCACCAG GGTGCCATGC
954 851 CGGCCTTCGC CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT
955 901 AGCCATCTGC AGAGCTTCCT GGAGGTGTCTG TACCGCGTTC TACGCCACCT
956 951 TGCGCAGCCC GACATGGCTA CACCA (SEQ ID NO:259);
957
958
959 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
960 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
961 101 CTATCCTGAT GGATCGAAAC CTTGCGACTTC CAAACCTGGA GAGCTTCGTA
962 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
963 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
964 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
965 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
966 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
967 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCAGAGC
968 451 TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC
969 501 AGCGCTCCAG GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCGAGG
970 551 AGCTGGTGCT GCTCGGACAC TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC
971 601 TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA GGCTGCTTGA GCCAACTCCA
972 651 TAGCGGCCTT TTCTCTACC AGGGGCTCCT GCAGGCCCTG GAAGGGATAT
973 701 CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC
974 751 TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC
975 801 CCTGCAGCCC ACCCAGGGTG CCATGCCGGC CTTGCTCTCT GCTTTCCAGC
976 851 GCCGGGCAGG AGGGGTCTCT GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG
977 901 GTGTCTGACC GCGTTCCTACG CCACCTTGCG CAGCCCGACA TGGCTACACC
978 951 ATTAGGCCCT GCCAGCTCCC TGCCC (SEQ ID NO:260);
979
980
981 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
982 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT

983	101	CTATCCTGAT	GGATCGAAAC	CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA
984	151	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	GGTATTGAGG	CAATTCTTCG
985	201	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	TCTCGACATC
986	251	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG
987	301	TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAGT	ACGTAGAGGG
988	351	CGGTGGAGGC	TCCCCGGGTG	AACCGTCTGG	TCCAATCTCT	ACTATCAACC
989	401	CGTCTCCTCC	GTCTAAAGAA	TCTCATAAAT	CTCCAAACAT	GGCTTTCCTG
990	451	CTCAAGTCTT	TAGAGCAAGT	GAGGAAGATC	CAGGGCGATG	GCGCAGCGCT
991	501	CCAGGAGAAG	CTGTGTGCCA	CCTACAAGCT	GTGCCACCCC	GAGGAGCTGG
992	551	TGCTGCTCGG	ACACTCTCTG	GGCATCCCCT	GGGCTCCCCT	GAGCTCCTGC
993	601	CCCAGCCAGG	CCCTGCAGCT	GGCAGGCTGC	TTGAGCCAAC	TCCATAGCGG
994	651	CCTTTTCCTC	TACCAGGGGC	TCCTGCAGGC	CCTGGAAGGG	ATATCCCCCG
995	701	AGTTGGGTCC	CACCTTGGAC	ACACTGCAGC	TGGACGTCGC	CGACTTTGCC
996	751	ACCACCATCT	GGCAGCAGAT	GGAAGAAGT	GGAATGGCCC	CTGCCCTGCA
997	801	GCCACCCAG	GGTGCCATGC	CGGCCTTCGC	CTCTGCTTTC	CAGCGCCGGG
998	851	CAGGAGGGGT	CCTGGTTGCT	AGCCATCTGC	AGAGCTTCCT	GGAGGTGTCG
999	901	TACCGCGTTC	TACGCCACCT	TGCGCAGCCC	GACATGGCTA	CACCATTAGG
1000	951	CCCTGCCAGC	TCCCTGCCCC	AGAGC (SEQ	ID NO:261);	
1001						
1002						
1003	1	ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG
1004	51	ACCACCTGCA	CCTTTGCTGG	ACCCGAACAA	CCTCAATGAC	GAAGACGTCT
1005	101	CTATCCTGAT	GGATCGAAAC	CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA
1006	151	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	GGTATTGAGG	CAATTCTTCG
1007	201	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	TCTCGACATC
1008	251	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG
1009	301	TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAGT	ACGTAGAGGG
1010	351	CGGTGGAGGC	TCCCCGGGTG	AACCGTCTGG	TCCAATCTCT	ACTATCAACC
1011	401	CGTCTCCTCC	GTCTAAAGAA	TCTCATAAAT	CTCCAAACAT	GGCTGAGCAA
1012	451	GTGAGGAAGA	TCCAGGGCGA	TGGCGCAGCG	CTCCAGGAGA	AGCTGTGTGC
1013	501	CACCTACAAG	CTGTGCCACC	CCGAGGAGCT	GGTGCTGCTC	GGACACTCTC
1014	551	TGGGCATCCC	CTGGGCTCCC	CTGAGCTCCT	GCCCCAGCCA	GGCCCTGCAG
1015	601	CTGGCAGGCT	GCTTGAGCCA	ACTCCATAGC	GGCCTTTTCC	TCTACCAGGG
1016	651	GCTCCTGCAG	GCCCTGGAAG	GGATATCCCC	CGAGTTGGGT	CCCACCTTGG
1017	701	ACACACTGCA	GCTGGACGTC	GCCGACTTTG	CCACCACCAT	CTGGCAGCAG
1018	751	ATGGAAGAAC	TGGGAATGGC	CCCTGCCCTG	CAGCCCACCC	AGGGTGCCAT
1019	801	GCCGGCCTTC	GCCTCTGCTT	TCCAGCGCCG	GGCAGGAGGG	GTCCTGGTTG
1020	851	CTAGCCATCT	GCAGAGCTTC	CTGGAGGTGT	CGTACCGCGT	TCTACGCCAC
1021	901	CTTGCGCAGC	CCGACATGGC	TACACCATTA	GGCCCTGCCA	GCTCCCTGCC
1022	951	CCAGAGCTTC	CTGCTCAAGT	CTTTA (SEQ	ID NO:262);	
1023						
1024						
1025	1	ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG
1026	51	ACCACCTGCA	CCTTTGCTGG	ACCCGAACAA	CCTCAATGAC	GAAGACGTCT
1027	101	CTATCCTGAT	GGATCGAAAC	CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA
1028	151	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	GGTATTGAGG	CAATTCTTCG
1029	201	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	TCTCGACATC

1030 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1031 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1032 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1033 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGCTC
 1034 451 GGACACTCTC TGGGCATCCC CTGGGCTCCC CTGAGCTCCT GCCCCAGCCA
 1035 501 GGCCCTGCAG CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCTTTTCC
 1036 551 TCTACCAGGG GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT
 1037 601 CCCACCTTGG ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT
 1038 651 CTGGCAGCAG ATGGAAGAAC TGGAATGGC CCCTGCCCTG CAGCCCACCC
 1039 701 AGGGTGCCAT GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG
 1040 751 GTCCTGGTTG CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT
 1041 801 TCTACGCCAC CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA
 1042 851 GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG
 1043 901 ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA
 1044 951 GCTGTGCCAC CCCGAGGAGC TGGTG (SEQ ID NO:263);
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 1046
 1047 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1048 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1049 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1050 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1051 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1052 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1053 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1054 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1055 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCCCCTG
 1056 451 AGCTCCTGCC CCAGCCAGGC CCTGCAGCTG GCAGGCTGCT TGAGCCAACT
 1057 501 CCATAGCGGC CTTTTCTCTT ACCAGGGGCT CCTGCAGGCC CTGGAAGGGA
 1058 551 TATCCCCCGA GTTGGGTCCC ACCTTGGACA CACTGCAGCT GGACGTCGCC
 1059 601 GACTTTGCCA CCACCATCTG GCAGCAGATG GAAGAACTGG GAATGGCCCC
 1060 651 TGCCCTGCAG CCCACCCAGG GTGCCATGCC GGCCTTCGCC TCTGCTTTCC
 1061 701 AGCGCCGGGC AGGAGGGGTC CTGGTTGCTA GCCATCTGCA GAGCTTCCTG
 1062 751 GAGGTGTCGT ACCGCGTTCT ACGCCACCTT GCGCAGCCCG ACATGGCTAC
 1063 801 ACCATTAGGC CCTGCCAGCT CCCTGCCCCA GAGCTTCCTG CTCAAGTCTT
 1064 851 TAGAGCAAGT GAGGAAGATC CAGGGCGATG GCGCAGCGCT CCAGGAGAAG
 1065 901 CTGTGTGCCA CCTACAAGCT GTGCCACCCC GAGGAGCTGG TGCTGCTCGG
 1066 951 AACTCTCTG GGCATCCCCT GGGCT (SEQ ID NO:264);
 1067
 1068
 1069 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1070 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1071 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1072 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1073 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1074 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1075 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1076 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC

1077 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCAGGCC
 1078 451 CTGCAGCTGG CAGGCTGCTT GAGCCAACTC CATAGCGGCC TTTTCCTCTA
 1079 501 CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG TTGGGTCCCA
 1080 551 CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG
 1081 601 CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG
 1082 651 TGCCATGCCG GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC
 1083 701 TGGTTGCTAG CCATCTGCAG AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA
 1084 751 CGCCACCTTG CGCAGCCCGA CATGGCTACA CCATTAGGCC CTGCCAGCTC
 1085 801 CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC
 1086 851 AGGGCGATGG CGCAGCGCTC CAGGAGAAGC TGTGTGCCAC CTACAAGCTG
 1087 901 TGCCACCCCG AGGAGCTGGT GCTGCTCGGA CACTCTCTGG GCATCCCCTG
 1088 951 GGCTCCCCTG AGCTCCTGCC CCAGC (SEQ ID NO:265);
 1089
 1090
 1091 1 ATGGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1092 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1093 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1094 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1095 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1096 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG
 1097 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1098 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1099 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGCAG
 1100 451 CTGGCAGGCT GCTTGAGCCA ACTCCATAGC GGCCTTTTCC TCTACCAGGG
 1101 501 GCTCCTGCAG GCCCTGGAAG GGATATCCCC CGAGTTGGGT CCCACCTTGG
 1102 551 ACACACTGCA GCTGGACGTC GCCGACTTTG CCACCACCAT CTGGCAGCAG
 1103 601 ATGGAAGAAC TGGGAATGGC CCCTGCCCTG CAGCCCACCC AGGGTGCCAT
 1104 651 GCCGGCCTTC GCCTCTGCTT TCCAGCGCCG GGCAGGAGGG GTCCTGGTTG
 1105 701 CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC
 1106 751 CTTGCGCAGC CCGACATGGC TACACCATTA GGCCCTGCCA GCTCCCTGCC
 1107 801 CCAGAGCTTC CTGCTCAAGT CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG
 1108 851 ATGGCGCAGC GCTCCAGGAG AAGCTGTGTG CCACCTACAA GCTGTGCCAC
 1109 901 CCCGAGGAGC TGGTGCTGCT CGGACACTCT CTGGGCATCC CCTGGGCTCC
 1110 951 CCTGAGCTCC TGCCCCAGCC AGGCC (SEQ ID NO:266);
 1111
 1112
 1113 1 ATGGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1114 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1115 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1116 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1117 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1118 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG
 1119 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1120 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1121 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTCTGGCA
 1122 451 GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT
 1123 501 GCAGGCCCTG GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC

1124 551 TGCAGCTGGA CGTCGCCGAC TTTGCCACCA CCATCTGGCA GCAGATGGAA
 1125 601 GAACTGGGAA TGGCCCCTGC CCTGCAGCCC ACCCAGGGTG CCATGCCGGC
 1126 651 CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTTG GTTGCTAGCC
 1127 701 ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG
 1128 751 CAGCCCGACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG
 1129 801 CTTCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG
 1130 851 CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCCGAG
 1131 901 GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG
 1132 951 CTCCTGCCCC AGCCAGGCC TGCAG (SEQ ID NO:267);
 1133
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 1135 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1136 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1137 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1138 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1139 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1140 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1141 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1142 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1143 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTGAACTG
 1144 451 GGAATGGCCC CTGCCCTGCA GCCCACCAG GGTGCCATGC CGGCCTTCGC
 1145 501 CTCTGCTTTC CAGCGCCGGG CAGGAGGGGT CCTGGTTGCT AGCCATCTGC
 1146 551 AGAGCTTCCT GGAGGTGTCG TACCGCGTTC TACGCCACCT TGCGCAGCCC
 1147 601 GACATGGCTA CACCATTAGG CCCTGCCAGC TCCCTGCCCC AGAGCTTCCT
 1148 651 GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT GGCGCAGCGC
 1149 701 TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG
 1150 751 GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG
 1151 801 CCCCAGCCAG GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG
 1152 851 GCCTTTTCCT CTACCAGGGG CTCCTGCAGG CCCTGGAAGG GATATCCCCC
 1153 901 GAGTTGGGTC CCACCTTGGA CACACTGCAG CTGGACGTCG CCGACTTTGC
 1154 951 CACCACCATC TGGCAGCAGA TGGAA (SEQ ID NO:268);
 1155
 1156
 1157 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1158 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1159 101 CTATCCTGAT GGATCGAAAC CTTGCACTTC CAAACCTGGA GAGCTTCGTA
 1160 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1161 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1162 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1163 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1164 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1165 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTGGAATG
 1166 451 GCCCCTGCCC TGCAGCCCAC CCAGGGTGCC ATGCCGGCCT TCGCCTCTGC
 1167 501 TTTCCAGCGC CGGGCAGGAG GGGTCTTGGT TGCTAGCCAT CTGCAGAGCT
 1168 551 TCCTGGAGGT GTCGTACCGC GTTCTACGCC ACCTTGCGCA GCCCGACATG
 1169 601 GCTACACCAT TAGGCCCTGC CAGCTCCCTG CCCCAGAGCT TCCTGCTCAA
 1170 651 GTCTTTAGAG CAAGTGAGGA AGATCCAGGG CGATGGCGCA GCGCTCCAGG

1171 701 AGAAGCTGTG TGCCACCTAC AAGCTGTGCC ACCCCGAGGA GCTGGTGCTG
 1172 751 CTCGGACACT CTCTGGGCAT CCCCTGGGCT CCCCTGAGCT CCTGCCCCAG
 1173 801 CCAGGCCCTG CAGCTGGCAG GCTGCTTGAG CCAACTCCAT AGCGGCCTTT
 1174 851 TCCTCTACCA GGGGCTCCTG CAGGCCCTGG AAGGGATATC CCCCAGATTG
 1175 901 GGTCACACCT TGGACACACT GCAGCTGGAC GTCGCCGACT TTGCCACCAC
 1176 951 CATCTGGCAG CAGATGGAAG AACTG (SEQ ID NO:269); and
 1177
 1178
 1179 1 ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG
 1180 51 ACCACCTGCA CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT
 1181 101 CTATCCTGAT GGATCGAAAC CTTCGACTTC CAAACCTGGA GAGCTTCGTA
 1182 151 AGGGCTGTCA AGAACTTAGA AAATGCATCA GGTATTGAGG CAATTCTTCG
 1183 201 TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC TCTCGACATC
 1184 251 CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG
 1185 301 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG
 1186 351 CGGTGGAGGC TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC
 1187 401 CGTCTCCTCC GTCTAAAGAA TCTCATAAAT CTCCAAACAT GGCTAGCTTC
 1188 451 CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC CCGACATGGC
 1189 501 TACACCATTA GGCCCTGCCA GCTCCCTGCC CCAGAGCTTC CTGCTCAAGT
 1190 551 CTTTAGAGCA AGTGAGGAAG ATCCAGGGCG ATGGCGCAGC GCTCCAGGAG
 1191 601 AAGCTGTGTG CCACCTACAA GCTGTGCCAC CCCGAGGAGC TGGTGCTGCT
 1192 651 CGGACACTCT CTGGGCATCC CCTGGGCTCC CCTGAGCTCC TGCCCCAGCC
 1193 701 AGGCCCTGCA GCTGGCAGGC TGCTTGAGCC AACTCCATAG CGGCCTTTTC
 1194 751 CTCTACCAGG GGCTCCTGCA GGCCCTGGAA GGGATATCCC CCGAGTTGGG
 1195 801 TCCCACCTTG GACACACTGC AGCTGGACGT CGCCGACTTT GCCACCACCA
 1196 851 TCTGGCAGCA GATGGAAGAA CTGGGAATGG CCCCTGCCCT GCAGCCCACC
 1197 901 CAGGGTGCCA TGCCGGCCTT CGCCTCTGCT TTCCAGCGCC GGGCAGGAGG
 1198 951 GGTCTGGTT GCTAGCCATC TGCAG (SEQ ID NO:270).

1 37. The nucleic acid molecule according to claim 34
 2 selected from group consisting of:
 3

4 1 ATGGCTGGAC CCACTTGCCT CTCATCCCTC CTGGGGCAGC TTTCTGGACA
 5 51 GTCCGTCTC CTCCTTGGGG CCCTGCAGAG CCTCCTTGGA ACCCAGCTTC
 6 101 CTCCACAGGG CAGGACCACA GCTCACAAGG ATCCCAATGC CATCTTCCTG
 7 151 AGCTTCCAAC ACCTGCTCCG AGGAAAGGTG CGTTTCCTGA TGCTTGTAGG
 8 201 AGGGTCCACC CTCGCCGTCA GGAATTCGG CGGCAACATG GCGTCTCCGG
 9 251 CGCCGCCTGC TGCTGACCTC CGAGTCCTCA GTAAACTGCT TCGTGACTCC
 10 301 CATGTCTTTC ACAGCAGACT GAGCCAGTGC CCAGAGGTTC ACCCTTTGCC
 11 351 TACACCTGTC CTGCTGCCTG CTGTGGACTT TAGCTTGGGA GAATGGAAAA
 12 401 CCCAGATGGA GGAGACCAAG GCACAGGACA TTCTGGGAGC AGTGACCCTT
 13 451 CTGCTGGAGG GAGTGATGGC AGCACGGGGA CAACTG
 14 (SEQ ID NO:286); and
 15
 16 1 ATGGCTGGCA GGACCACAGC TCACAAGGAT CCCAATGCCA TCTTCCTGAG
 17 51 CTTCCAACAC CTGCTCCGAG GAAAGGTGCG TTTCTTGATG CTTGTAGGAG
 18 101 GTCCACCCT CGCCGTCAGG GAATTCGGCG GCAACATGGC GTCTCCGGCG

19 151 CCGCCTGCTG CTGACCTCCG AGTCCTCAGT AACTGCTTC GTGACTCCCA
20 201 TGTCCTTCAC AGCAGACTGA GCCAGTGCCC AGAGGTTTAC CCTTTGCCTA
21 251 CACCTGTCCT GCTGCCTGCT GTGGACTTTA GCTTGGGAGA ATGGAAAACC
22 301 CAGATGGAGG AGACCAAGGC ACAGGACATT CTGGGAGCAG TGACCCTTCT
23 351 GCTGGAGGGA GTGATGGCAG CACGGGGACA ACTGGGACCC ACTTGCCTCT
24 401 CATCCCTCCT GGGGCAGCTT TCTGGACAGG TCCGTCTCCT CCTTGGGGCC
25 451 CTGCAGAGCC TCCTTGAAC CCAGCTTCCT CCACAG
26 (SEQ ID NO:287).

1 38. A method of producing a hematopoietic protein
2 comprising: growing under suitable nutrient conditions, a host
3 cell transformed or transfected with a replicable vector
4 comprising a nucleic acid molecule of claim 20, 21, 22, 23,
5 24, 25, 26, 27, 28, 30, 33, 34, 36 or 37 in a manner allowing
6 expression of said hematopoietic protein and recovering said
7 hematopoietic protein.

1 39. A pharmaceutical composition comprising; the
2 hematopoietic protein according to claim 1, 2, 3, 4, 5, 6, 7,
3 8, 9, 10, 12, 15 or 16 and a pharmaceutically acceptable
4 carrier.

1 40. A method of stimulating the production of
2 hematopoietic cells in a patient comprising the step of;
3 administering an effective amount of the hematopoietic protein
4 as recited in claim 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, or
5 16 to said patient.

1 41. A method of stimulating the production of
2 hematopoietic cells in a patient comprising the step of
3 administering an effective amount of the hematopoietic protein
4 as recited in claim 13 to said patient.

1 42. A method for selective ex vivo expansion of stem
2 cells, comprising the steps of:

3 (a) separating stem cells from other cells;

4 (b) culturing said separated stem cells with a selected
5 culture medium comprising; the hematopoietic protein of claim
6 1; and

7 (c) harvesting said cultured cells.

1 43. A method for treatment of a patient having a
2 hematopoietic disorder, comprising the steps of:

3 (a) removing stem cells;

4 (b) separating stem cells from other cells;

5 (c) culturing said separated stem cells with a selected
6 culture medium comprising; the hematopoietic protein of claim
7 1;

8 (d) harvesting said cultured cells; and

9 (e) transplanting said cultured cells into said patient.

1 44. A method of human gene therapy, comprising the steps
2 of:

3 (a) removing stem cells from a patient;

4 (b) separating said stem cells from other cells;

5 (c) culturing said separated stem cells with a selected
6 culture medium comprising; the hematopoietic protein of claim
7 1;

8 (d) introducing DNA into said cultured cells;

9 (e) harvesting said transduced cells; and

10 (f) transplanting said transduced cells into said
11 patient.

1 45. A method of human gene therapy, comprising the steps
2 of:

3 (a) removing stem cells from a patient;

4 (b) separating said stem cells from other cells;

5 (c) culturing said separated stem cells with a selected
6 culture medium comprising; the hematopoietic protein of claim
7 1;

8 (d) introducing DNA into said cultured cells;

9 (e) harvesting said transduced cells; and

10 (f) transplanting said transduced cells into said
11 patient.

1 46. A method of human gene therapy, comprising the steps
2 of:
3 (a) removing stem cells from a patient;
4 (b) separating said stem cells from other cells;
5 (c) culturing said separated stem cells with a selected
6 culture medium comprising; the hematopoietic protein of claim
7 11;
8 (d) introducing DNA into said cultured cells;
9 (e) harvesting said transduced cells; and
10 (f) transplanting said transduced cells into said
11 patient.

1 47. A method of human gene therapy, comprising the steps
2 of:
3 (a) removing stem cells from a patient;
4 (b) separating said stem cells from other cells;
5 (c) culturing said separated stem cells with a selected
6 culture medium comprising; the hematopoietic protein of claim
7 11;
8 (d) introducing DNA into said cultured cells;
9 (e) harvesting said transduced cells; and
10 (f) transplanting said transduced cells into said
11 patient.